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# SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Burton, Dennis R
                  Barbas, Carlos F
                  Lerner, Richard A

    (ii) TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
           TO HUMAN IMMUNODEFICIENCY VIRUS

    (iii) NUMBER OF SEQUENCES: 170

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: The Scripps Research Institute, Office of
            Patent Counsel
        (B) STREET: 10666 North Torrey Pines Road, Suite 220,
            Mail Drop TPC8
        (C) CITY: La Jolla
        (D) STATE: CA
        (E) COUNTRY: USA
        (F) ZIP: 92037

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: 08/899,575
        (B) FILING DATE: 24-JUL-1997
        (C) CLASSIFICATION: 435

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/276,852
        (B) FILING DATE: 18-JUL-1994

        (A) APPLICATION NUMBER: US 08/178,302
        (B) FILING DATE: 30-SEP-1993

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 07/954,148
        (B) FILING DATE: 30-SEP-1992

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Fitting, Thomas
        (B) REGISTRATION NUMBER: 34,163
        (C) REFERENCE/DOCKET NUMBER: TSRI 313.2

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 619-554-2937
        (B) TELEFAX: 619-554-6312

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 173 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGCCGCAAAT TCTATTTCAA GGAGACAGTC ATAATGAAAT ACCTATTGCC TACGGCAGCC        60

GCTGGATTGT TATTACTCGC TGCCCAACCA GCCATGGCCC AGGTGAAACT GCTCGAGATT       120

TCTAGACTAG TTACCCGTAC GACGTTCCGG ACTACGGTTC TTAATAGAAT TCG             173
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 173 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
TCGACGAATT CTATTAAGAA CCGTAGTCCG GAACGTCGTA CGGGTAACTA GTCTAGAAAT        60

CTCGAGCAGT TTCACCTGGG CCATGGCTGG TTGGGCAGCG AGTAATAACA ATCCAGCGGC       120

TGCCGTAGGC AATAGGTATT TCATTATGAC TGTCTCCTTG AAATAGAATT TGC             173
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 131 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAATTCTAA ACTAGTCGCC AAGGAGACAG TCATAATGAA ATACCTATTG CCTACGGCAG     60

CCGCTGGATT GTTATTACTC GCTGCCCAAC CAGCCATGGC CGAGCTCGTC AGTTCTAGAG    120

TTAAGCGGCC G                                                        131

(2) INFORMATION FOR SEQ ID NO:4:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 139 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCGACGGCCG CTTAACTCTA GAACTGACGA GCTCGGCCAT GGCTGGTTGG GCAGCGAGTA     60

ATAACAATCC AGCGGCTGCC GTAGGCAATA GGTATTTCAT TATGACTGTC TCCTTGGCGA    120

CTAGTTTAGA ATTCAAGCT                                                 139

(2) INFORMATION FOR SEQ ID NO:5:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1               5                   10                  15

Ala Gln Pro Ala Met Ala Gln Val Lys Leu
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1               5                   10                  15

Ala Gln Pro Ala Met Ala Glu
            20
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA     60

CACAGGAGGA AGGATCCATG AAATACCTAT TGCCTACGGC AGCCGCTGGA TTGTTATTAC    120

TCGCTGCCCA ACCAGCCATG GCCGAGCTCG GTCGGTCGGT CCTCGAGGGT CGGTCGGTCT    180

CTAGAGTTAA GCGGCCGC                                                  198
```

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GCGGCCGCTT AACTCTAGAG ACCGACCGAC CCTCGAGGAC CGACCGACCG AGCTCGGCCA     60

TGGCTGGTTG GGCAGCGAGT AATAACAATC CAGCGGCTGC CGTAGGCAAT AGGTATTTCA    120

TGGATCCTTC CTCCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAT TATACGAGCC    180

GATGATTAAT TGTCAACA                                                  198
```

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (v) FRAGMENT TYPE: N-terminal

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Thr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1                   5                   10                  15

Ala Gln Pro Ala Met Ala Glu Leu
            20

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 220 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA     60

CACAGGAGGA AGGATCCATG AAATACCTAT TGCCTACGGC AGCCGCTGGA TTGTTATTAC    120

TCGCTGCCCA ACCAGCCATG GCCCAGGTGA AACTGCTCGA GGGTCGGTCG GTCTCTAGAC    180

GGTCGGTCGG TCACTAGTCA TCATCATCAT CATTAAGCTA                          220

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 220 base pairs
        (B) TYPE: nucleic acid

```
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: circular

            (ii) MOLECULE TYPE: DNA (genomic)

            (iii) HYPOTHETICAL: NO

            (iv) ANTI-SENSE: NO



            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAGCTTAATG ATGATGATGA TGACTAGTGA CCGACCGACC GTCTAGAGAC CGACCGACCC        60

TCGAGCAGTT TCACCTGGGC CATGGCTGGT TGGGCAGCGA GTAATAACAA TCCAGCGGCT       120

GCCGTAGGCA ATAGGTATTT CATGGATCCT TCCTCCTGTG TGAAATTGTT ATCCGCTCAC       180

AATTCCACAC ATTATACGAG CCGATGATTA ATTGTCAACA                            220
```

(2) INFORMATION FOR SEQ ID NO:13:

```
            (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 28 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: peptide

            (v) FRAGMENT TYPE: N-terminal



            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Lys Thr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1               5                   10                  15

Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:14:

```
            (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 7 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: peptide

            (v) FRAGMENT TYPE: C-terminal
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Ser His His His His His
1               5

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCCGCAAAT TCTATTTCAA GGAGACAGTC AT                32

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGAAATAC CTATTGCCTA CGGCAGCCGC TGGATT           36

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTTATTACTC GCTGCCCAAC CAGCCATGGC CC                                          32

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGTTTCACC TGGGCCATGG CTGGTTGGG                                              29

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGCGAGTAA TAACAATCCA GCGGCTGCCG TAGGCAATAG        40

(2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 38 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTATTTCATT ATGACTGTCT CCTTGAAATA GAATTTGC        38

(2) INFORMATION FOR SEQ ID NO:21:

     (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 40 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGGTGAAACT GCTCGAGATT TCTAGACTAG TTACCCGTAC        40

(2) INFORMATION FOR SEQ ID NO:22:

     (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 38 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGGAACGTCG TACGGGTAAC TAGTCTAGAA ATCTCGAG                    38

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 33 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

 (iii) HYPOTHETICAL: NO

 (iv) ANTI-SENSE: NO


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACGTTCCGG ACTACGGTTC TTAATAGAAT TCG                         33

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 28 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

 (iii) HYPOTHETICAL: NO

 (iv) ANTI-SENSE: NO


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCGACGAATT CTATTAAGAA CCGTAGTC                               28

(2) INFORMATION FOR SEQ ID NO:25:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 34 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGAATTCTAA ACTAGTCGCC AAGGAGACAG TCAT                                    34

(2) INFORMATION FOR SEQ ID NO:26:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 36 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATGAAATAC CTATTGCCTA CGGCAGCCGC TGGATT                                  36

(2) INFORMATION FOR SEQ ID NO:27:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 31 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTTATTACTC GCTGCCCAAC CAGCCATGGC C                                          31

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAGCTCGTCA GTTCTAGAGT TAAGCGGCCG                                            30

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTATTTCATT ATGACTGTCT CCTTGGCGAC TAGTTTAGAA TTCAAGCT                        48

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGCGAGTAA TAACAATCCA GCGGCTGCCG TAGGCAATAG          40

(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGACGAGCTC GGCCATGGCT GGTTGGG          27

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCGACGGCCG CTTAACTCTA GAAC          24

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 666 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
CCATTCGTTT GTGAATATCA AGGCCAAGGC CAATCGTCTG ACCTGCCTCA ACCTCCTGTC      60

AATGCTGGCG GCGGCTCTGG TGGTGGTTCT GGTGGCGGCT CTGAGGGTGG TGGCTCTGAG     120

GGTGGCGGTT CTGAGGGTGG CGGCTCTGAG GGAGGCGGTT CCGGTGGTGG CTCTGGTTCC     180

GGTGATTTTG ATTATGAAAA GATGGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCC     240

GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC     300

GGTGCTGCTA TCGATGGTTT CATTGGTGAC GTTTCCGGCC TTGCTAATGG TAATGGTGCT     360

ACTGGTGATT TTGCTGGCTC TAATTCCCAA ATGGCTCAAG TCGGTGACGG TGATAATTCA     420

CCTTTAATGA ATAATTTCCG TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC     480

CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC     540

TTATTCGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG     600

TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GGTATTCCGT     660

TATTAT                                                               666
```

(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 211 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: protein

    (iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Pro Phe Val Cys Glu Tyr Gln Gly Gln Gly Gln Ser Ser Asp Leu Pro
1               5               10              15

Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
            20              25              30

Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
        35              40              45

Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp
    50              55              60

Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala
65              70              75              80

Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val
            85              90              95

Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser
            100             105             110

Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn
        115             120             125

Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn
    130             135             140

Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg
145             150             155             160

Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys
            165             170             175

Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val
            180             185             190

Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn
        195             200             205

Lys Glu Ser
    210
```

(2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 base pairs

          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAGACGACTA GTGGTGGCGG TGGCTCTCCA TTCGTTTGTG AATATCAA                    48

(2) INFORMATION FOR SEQ ID NO:36:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 40 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTACTAGCTA GCATAATAAC GGAATACCCA AAAGAACTGG                    40

(2) INFORMATION FOR SEQ ID NO:37:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 36 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TATGCTAGCT AGTAACACGA CAGGTTTCCC GACTGG                          36

(2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCGAGCTCG AATTCGTAAT CATGGTC                          27

(2) INFORMATION FOR SEQ ID NO:39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCTGTTGAA TTCGTGAAAT TGTTATCCGC T                          31

(2) INFORMATION FOR SEQ ID NO:40:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 708 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGACGACTA GTGGTGGCGG TGGCTCTCCA TTCGTTTGTG AATATCAAGG CCAAGGCCAA      60

TCGTCTGACC TGCCTCAACC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGGTTCTGGT      120

GGCGGCTCTG AGGGTGGTGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGA      180

GGCGGTTCCG GTGGTGGCTC TGGTTCCGGT GATTTTGATT ATGAAAGAT GGCAAACGCT       240

AATAAGGGGG CTATGACCGA AAATGCCGAT GAAAACGCGC TACAGTCTGA CGCTAAAGGC      300

AAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT      360

TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAATG      420

GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTTACCT      480

TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA ACCATATGAA      540

TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT TCTTTTATAT      600

GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT      660

TAATCATGCC AGTTCTTTTG GGTATTCCGT TATTATGCTA GCTAGTAA               708

(2) INFORMATION FOR SEQ ID NO:41:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 201 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TATGCTAGCT AGTAACACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA GCGCAACGCA          60

ATTAATGTGA GTTAGCTCAC TCATTAGGCA CCCCAGGCTT TACACTTTAT GCTTCCGGCT         120

CGTATGTTGT GTGGAATTGT GAGCGGATAA CAATTTCACA CAGGAAACAG CTATGACCAT         180

GATTACGAAT TCGAGCTCGG T                                                   201

(2) INFORMATION FOR SEQ ID NO:42:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGGTGCAGC TCGAGCAGTC TGGG                                                 24

(2) INFORMATION FOR SEQ ID NO:43:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAGGTGCAGC TCGAGGAGTC TGGG                                                 24

(2) INFORMATION FOR SEQ ID NO:44:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs

            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCATGTACTA GTTTTGTCAC AAGATTTGGG                                30

(2) INFORMATION FOR SEQ ID NO:45:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GACATCGAGC TCACCCAGTC TCCA                                    24

(2) INFORMATION FOR SEQ ID NO:46:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAAATTGAGC TCACGCAGTC TCCA                                        24

(2) INFORMATION FOR SEQ ID NO:47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 53 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCGCCGTCTA GAACTAACAC TCTCCCCTGT TGAAGCTCTT TGTGACGGGC AAG          53

(2) INFORMATION FOR SEQ ID NO:48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: peptide

    (v) FRAGMENT TYPE: internal


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

   Ser Ile Ser Gly Pro Gly Arg Ala Phe Tyr Thr Gly
   1               5                   10

(2) INFORMATION FOR SEQ ID NO:49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTCGTTGACC AGGCAGCCCA G                                                    21

(2) INFORMATION FOR SEQ ID NO:50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATAGAAGTTG TTCAGCAGGC A                                                    21

(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATTAACCCTC ACTAAAG                                                         17

(2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATTCTAAA CTAGCTAGTT CG                                                  22

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Leu Glu Glu Ser Gly Thr Glu Phe Lys Pro Pro Gly Ser Ser Val Lys
1               5               10              15

Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gly Asp Tyr Ala Ser Asn
            20              25              30

Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr
        35              40              45

Ile Gly Gly Ile Thr Pro Thr Ser Gly Ser Ala Asp Tyr Ala Gln Lys
    50              55              60

Phe Gln Gly Arg Val Thr Ile Ser Ala Asp Arg Phe Thr Pro Ile Leu
65              70              75              80

Tyr Met Glu Leu Arg Ser Leu Arg Ile Glu Asp Thr Ala Ile Tyr Tyr
            85              90              95

Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Arg
            100             105             110

Gly Ala Leu Asp Phe Trp Gly Gln Gly Thr Arg Val Phe Val Ser Pro
        115                 120                 125


(2) INFORMATION FOR SEQ ID NO:54:

    (i)  SEQUENCE CHARACTERISTICS:
         (A)  LENGTH: 124 amino acids
         (B)  TYPE: amino acid
         (D)  TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

    Leu Glu Glu Ser Gly Ala Ala Val Gln Lys Pro Gly Ser Ser Val Arg
    1               5                   10                  15

    Val Ser Cys Gln Ala Ser Gly Gly Thr Phe Asp Asn Phe Ala Ser Asn
                20                  25                  30

    Tyr Ala Val Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            35                  40                  45

    Met Gly Gly Ile Thr Pro Thr Ser Gly Thr Ala Thr Tyr Ser Gln Lys
        50                  55                  60

    Phe Gln Gly Arg Val Thr Ile Ser Ala Ala Pro Leu Thr Pro Ile Ile
    65              70                  75                  80

    Tyr Met Glu Leu Arg Ser Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr
                85                  90                  95

    Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Val
                100                 105                 110

    Gly Ala Leu Asp Val Trp Gly Gln Gly Thr Thr Val
            115                 120

(2) INFORMATION FOR SEQ ID NO:55:

    (i)  SEQUENCE CHARACTERISTICS:
         (A)  LENGTH: 128 amino acids
         (B)  TYPE: amino acid
         (D)  TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Leu Glu Glu Ser Gly Thr Glu Phe Lys Pro Pro Gly Ser Ser Val Lys
1               5               10              15

Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gly Asp Tyr Ala Ser Asn
        20              25              30

Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr
        35              40              45

Ile Gly Gly Ile Thr Pro Thr Ser Gly Ser Ala Asp Tyr Ala Gln Lys
        50              55              60

Phe Gln Gly Arg Val Thr Ile Ser Ala Asp Arg Phe Thr Pro Ile Leu
65              70              75              80

Tyr Met Glu Leu Arg Ser Leu Arg Ile Glu Asp Thr Ala Ile Tyr Tyr
            85              90              95

Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Arg
            100             105             110

Gly Ala Leu Asp Phe Trp Gly Gln Gly Thr Arg Val Phe Val Ser Pro
            115             120             125


(2) INFORMATION FOR SEQ ID NO:56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Leu Glu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
1               5               10              15

Val Ser Cys Lys Ala Ser Gly Gly Ile Phe Ser Asp Phe Ala Ser Asn
        20              25              30

Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr
        35              40              45

Met Gly Gly Ile Thr Pro Thr Ser Gly Ser Ala Asp Tyr Ala Gln Lys
        50              55              60

```
     Phe Gln Gly Arg Val Thr Ile Ser Ala Asp Ala Ala Thr Pro Arg Val
     65              70              75                      80

     Tyr Met Glu Leu Arg Ile Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
                 85              90                      95

     Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Arg
                 100             105             110

     Gly Ala Leu Glu Val Trp Gly Gln Gly Thr Thr Val Ile Val Ser Pro
                 115             120             125
```

(2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 128 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
     Leu Glu Glu Ser Gly Ala Ala Val Gln Lys Pro Gly Ser Ser Val Arg
     1               5               10                      15

     Val Ser Cys Gln Ala Ser Gly Gly Thr Phe Asp Asn Phe Ala Ser Asn
                 20              25              30

     Tyr Ala Val Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
                 35              40              45

     Met Gly Gly Ile Thr Pro Thr Ser Gly Thr Ala Thr Tyr Ser Gln Lys
         50              55              60

     Phe Gln Gly Arg Val Thr Ile Ser Ala Ala Pro Leu Thr Pro Ile Ile
     65              70              75                      80

     Tyr Met Glu Leu Arg Ser Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr
                 85              90                      95

     Cys Ala Arg Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Val
                 100             105             110

     Gly Ala Leu Asp Val Trp Gly Gln Gly Thr Thr Val Ile Val Ser Ser
                 115             120             125
```


(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 128 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
1             5                   10                  15

Val Ser Cys Lys Thr Ser Gly Gly Thr Phe Ser Asp Tyr Ala Ser Asn
            20                  25                  30

His Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Tyr
            35                  40                  45

Met Gly Gly Ile Thr Pro Thr Ser Gly Thr Ala Asp Tyr Ala Gln Lys
    50                  55                  60

Phe Gln Ala Arg Val Thr Ile Ser Ala His Glu Phe Thr Pro Ile Val
65                  70                  75                  80

Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Gln His Ala Thr Tyr Tyr
            85                  90                  95

Cys Ala Thr Glu Arg Arg Glu Arg Gly Trp Asn Pro Arg Ala Leu Arg
            100                 105                 110

Gly Ala Leu Asp Ile Trp Gly Gln Gly Thr Thr Val Ile Val Ser Ser
            115                 120                 125
```


(2) INFORMATION FOR SEQ ID NO:59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
Leu Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Gly Gly Ser Leu Arg
1             5                   10                  15
```

```
Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
            20              25              30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
        35              40              45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
    50              55              60

Gly Arg Phe Ser Ile Ser Arg Asn Asp Leu Glu Asp Lys Met Phe Leu
65              70              75              80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
            85              90              95

Thr Lys Tyr Pro Arg Tyr Ser Asp Met Val Thr Gly Val Arg Asn His
            100             105             110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
            115             120             125
```

(2) INFORMATION FOR SEQ ID NO:60:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Leu Glu Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5               10              15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
            20              25              30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
        35              40              45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
    50              55              60

Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Leu Phe Leu
65              70              75              80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
            85              90              95
```

```
      Thr Lys Tyr Pro Arg Tyr Phe Asp Met Met Ala Gly Val Arg Asn His
              100             105             110

      Phe Tyr Met Asp Val Trp Gly Thr Gly Thr Thr Val Ile Val Ser Ser
          115             120             125
```

(2) INFORMATION FOR SEQ ID NO:61:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
   Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
   1               5                   10              15

   Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
              20              25              30

   Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
          35              40              45

   Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
       50              55              60

   Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Leu Phe Leu
   65              70              75              80

   Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
              85              90              95

   Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Ala Gly Val Arg Asn His
          100             105             110

   Leu Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
       115             120             125
```

(2) INFORMATION FOR SEQ ID NO:62:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Leu Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Thr Asn Ser Trp Met Thr
            20                  25                  30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
        35                  40                  45

Lys Arg Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
        50                  55                  60

Gly Arg Phe Ser Ile Ser Arg Asn Asp Leu Glu Asp Lys Met Phe Leu
65                  70                  75                  80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
                85                  90                  95

Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Thr Gly Val Arg Asn His
            100                 105                 110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
            115                 120                 125
```


(2) INFORMATION FOR SEQ ID NO:63:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 128 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Glu Ser Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
            20                  25                  30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
        35                  40                  45
```

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
    50              55              60

Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Leu Phe Leu
65              70              75              80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
            85              90              95

Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Ala Gly Val Arg Asn His
            100             105             110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
        115             120             125


(2) INFORMATION FOR SEQ ID NO:64:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Glu Glu Ser Gly Gly Arg Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5               10              15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
            20              25              30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
            35              40              45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
    50              55              60

Gly Arg Phe Ser Ile Ser Arg Asn Asp Leu Glu Asp Lys Met Phe Leu
65              70              75              80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
            85              90              95

Thr Lys Tyr Pro Arg Tyr Ser Asp Met Met Thr Gly Val Arg Asn His
            100             105             110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
        115             120             125

(2) INFORMATION FOR SEQ ID NO:65:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Thr Asn Ala Trp Met Thr
            20                  25                  30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
            35                  40                  45

Lys Ser Lys Phe Asp Gly Gly Ser Ser His Tyr Pro Gly Pro Val Glu
        50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asn Tyr Ile Glu Asp Lys Leu Phe Leu
65                  70                  75                  80

Glu Met Ser Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
                85                  90                  95

Thr Lys Tyr Pro Arg Tyr Tyr Asp Met Met Arg Gly Val Arg Asn His
            100                 105                 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
            115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:66:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
1               5               10                  15

Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe Val Ile His
            20              25                  30

Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp Met Gly Trp Ile
        35              40                  45

Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg
        50              55                  60

Val Thr Phe Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr Met Glu Leu
65              70                  75                  80

Arg Ser Leu Arg Ser Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val
                85              90                  95

Gly Pro Tyr Ser Trp Asp Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp
                100             105                 110

Val Trp Gly Lys Gly Thr Thr Val Ile Val Ser Ser
            115             120
```

(2) INFORMATION FOR SEQ ID NO:67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
1               5               10                  15

Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe Val Ile His
            20              25                  30

Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp Met Gly Trp Ile
        35              40                  45

Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg
        50              55                  60

Val Thr Phe Thr Ala Asp Thr Asp Ala Asn Thr Ala Tyr Met Glu Leu
65              70                  75                  80
```

```
    Arg Ser Leu Arg Ser Ala Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Val
                85                  90                  95

    Gly Pro Tyr Thr Trp Asp Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp
                100                 105                 110

    Val Trp Gly Lys Gly Thr Lys Val Ile Val Ser Ser
                115                 120
```

(2) INFORMATION FOR SEQ ID NO:68:

    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 124 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
    Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
    1               5                   10                  15

    Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn Phe Val Ile His
                20                  25                  30

    Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp Met Gly Trp Ile
                35                  40                  45

    Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg
        50                  55                  60

    Val Thr Phe Thr Ala Asp Thr Asp Ala Asn Thr Ala Tyr Met Glu Leu
    65                  70                  75                  80

    Arg Ser Leu Arg Ser Thr Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Val
                85                  90                  95

    Gly Pro Tyr Thr Trp Asp Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp
                100                 105                 110

    Val Trp Gly Lys Gly Thr Lys Val Ile Val Ser Ser
                115                 120
```

(2) INFORMATION FOR SEQ ID NO:69:

    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 130 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Val Gly Ser Gly Phe Thr Phe Ser Ser Ala Trp Met Ala
            20                  25                  30

Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Gly Leu Ile
        35                  40                  45

Lys Ser Lys Ala Asp Gly Glu Thr Thr Asp Tyr Ala Thr Pro Val Lys
    50                  55                  60

Gly Arg Phe Ser Ile Ser Arg Asn Asn Leu Glu Asp Thr Val Tyr Leu
65                  70                  75                  80

Gln Met Asp Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Thr Gln Lys Pro Arg Tyr Phe Asp Leu Leu Ser Gly Gln Tyr Arg Arg
            100                 105                 110

Val Ala Gly Ala Phe Asp Val Trp Gly His Gly Thr Thr Val Thr Val
            115                 120                 125

Ser Pro
130

(2) INFORMATION FOR SEQ ID NO:70:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 130 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Ala Gly Gly Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Val Gly Ser Gly Phe Thr Phe Ser Ser Ala Trp Met Ala
            20                  25                  30

```
Trp Val Gly Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Gly Leu Ile
        35              40              45

Lys Ser Lys Ala Asp Gly Glu Thr Thr Asp Tyr Ala Thr Pro Val Lys
    50              55              60

Gly Arg Phe Ser Ile Ser Arg Asn Asn Leu Glu Asp Thr Val Tyr Leu
65              70              75                      80

Gln Met Asp Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala
                85              90                      95

Thr Gln Lys Pro Arg Tyr Phe Asp Leu Leu Ser Gly Gln Tyr Arg Arg
                100             105             110

Val Ala Gly Ala Phe Asp Val Trp Gly His Gly Thr Thr Val Thr Val
        115             120             125

Ser Pro
130
```

(2) INFORMATION FOR SEQ ID NO:71:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 130 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
Leu Glu Glu Ser Gly Gly Gly Leu Ile Lys Pro Gly Gly Ser Leu Arg
1               5               10              15

Leu Ser Cys Val Gly Ser Gly Phe Thr Phe Ser Ser Ala Trp Met Thr
        20              25              30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Leu Ile
        35              40              45

Lys Ser Lys Ala Asp Gly Glu Thr Thr Asp Tyr Ala Thr Pro Val Lys
    50              55              60

Gly Arg Phe Thr Ile Ser Arg Asn Asn Leu Glu Asn Thr Val Tyr Leu
65              70              75                      80

Gln Met Asp Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala
                85              90                      95
```

Thr Gln Lys Pro Ser Tyr Tyr Asn Leu Leu Ser Gly Gln Tyr Arg Arg
        100                     105                 110

Val Ala Gly Ala Phe Asp Val Trp Gly His Gly Thr Thr Val Thr Val
        115                     120                 125

Ser Pro


(2) INFORMATION FOR SEQ ID NO:72:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

    Leu Glu Glu Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg
    1               5                   10                  15

    Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Asn Tyr Ala Met His
            20                  25                  30

    Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
            35                  40                  45

    Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
        50                  55                  60

    Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
    65                  70                  75                  80

    Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
                85                  90                  95

    Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro
                100                 105                 110

    Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                115                 120                 125

(2) INFORMATION FOR SEQ ID NO:73:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Thr Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met His
            20                  25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
            35                  40                  45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
        50                  55                  60

Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Glu Met
65                  70                  75                  80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
            85                  90                  95

Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Ala Leu Val Thr Val Ser Ser
        115                 120                 125

(2) INFORMATION FOR SEQ ID NO:74:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Asn Tyr Ala Met His
            20                  25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
            35                  40                  45

```
Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
    50                  55                  60

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
65                  70                  75                  80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
                85                  90                  95

Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro
                100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:75:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
Leu Glu Glu Ser Gly Glu Ala Val Val Gln Pro Gly Thr Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met His
                20                  25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
                35                  40                  45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
    50                  55                  60

Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Glu Met
65                  70                  75                  80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
                85                  90                  95

Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro
                100                 105                 110

Asp Tyr Trp Gly Gln Gly Ala Leu Val Thr Val Ser Ser
                115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met His
        20                  25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
        35                  40                  45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
    50                  55                  60

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
65                  70                  75                  80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
                85                  90                  95

Ile Gly Leu Lys Ala Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:77:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
Leu Glu Gln Ser Gly Glu Ala Val Val Gln Pro Gly Arg Ser Leu Arg
1               5                   10                  15
```

```
Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Asn Tyr Ala Met His
        20              25              30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile
        35              40              45

Lys Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
        50              55              60

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
65              70              75              80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
                85              90              95

Ile Gly Leu Lys Gly Glu His Tyr Asp Ile Leu Thr Ala Tyr Gly Pro
            100             105             110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            115             120             125
```

(2) INFORMATION FOR SEQ ID NO:78:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
Leu Glu Gln Ser Gly Gly Gly Val Val Lys Pro Gly Gly Ser Leu Arg
1               5               10              15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Pro Asn Ala Trp Met Thr
        20              25              30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
        35              40              45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
        50              55              60

Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Val Phe Leu
65              70              75              80

Gln Met Asn Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
            85              90              95
```

```
Thr Arg Tyr Pro Arg Tyr Ser Glu Met Met Gly Gly Val Arg Lys His
            100             105             110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ser Val Ser Ser
            115             120             125
```

(2) INFORMATION FOR SEQ ID NO:79:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
Leu Glu Glu Ser Gly Gly Gly Val Val Lys Pro Gly Gly Ser Leu Arg
1               5               10              15

Leu Ser Cys Glu Gly Ser Gly Phe Thr Phe Pro Asn Ala Trp Met Thr
            20              25              30

Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile
            35              40              45

Lys Ser Lys Phe Asp Gly Gly Ser Pro His Tyr Ala Ala Pro Val Glu
            50              55              60

Gly Arg Phe Thr Ile Ser Arg Asn Asp Leu Glu Asp Lys Val Phe Leu
65                  70              75                  80

Gln Met Asn Gly Leu Lys Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
                85              90                  95

Thr Arg Tyr Pro Arg Tyr Ser Glu Met Met Gly Gly Val Arg Lys His
            100             105             110

Phe Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ser Val Ser Ser
            115             120             125
```

(2) INFORMATION FOR SEQ ID NO:80:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 122 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg
1               5                   10                  15

Val Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Ser Tyr Glu Met Asn
            20                  25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gln Ile
            35                  40                  45

Ser Ser Ser Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
    50                  55                  60

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Glu Met
65                  70                  75                  80

Thr Ser Leu Arg Val Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
            85                  90                  95

Arg Arg Leu Val Thr Phe Gly Gly Val Val Ser Gly Gly Asn Ile Trp
            100                 105                 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
            115                 120
```

(2) INFORMATION FOR SEQ ID NO:81:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 126 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
Leu Glu Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
1               5                   10                  15

Leu Ser Cys Ala Gly Ser Gly Phe Asn Phe Ser Asp Asp Thr Met His
            20                  25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
            35                  40                  45
```

```
Ser Tyr Glu Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
 50              55              60

Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr Leu Gln Met
65              70              75              80

Asp Ser Leu Arg Ala Asp Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Asn
            85              90              95

Thr Arg Glu Asn Ile Glu Ala Asp Gly Thr Ala Tyr Tyr Ser Tyr Tyr
            100             105             110

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
    115             120             125
```

(2) INFORMATION FOR SEQ ID NO:82:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 107 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5               10              15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala
            20              25              30

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Arg Leu Leu Ile Tyr Ala
        35              40              45

Ala Ser Thr Leu Gln Pro Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50              55              60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65              70              75              80

Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Arg Thr Phe
            85              90              95

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100             105
```

(2) INFORMATION FOR SEQ ID NO:83:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 106 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

    Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
    1               5               10              15

    Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala
                20              25              30

    Trp Tyr Gln Gln Arg Pro Gly Lys Val Pro Arg Leu Leu Ile Tyr Ala
            35              40              45

    Ala Ser Thr Leu Gln Ser Gly Val Pro Thr Arg Phe Ser Gly Ser Gly
        50              55              60

    Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    65              70              75              80

    Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro Arg Thr Phe
                85              90              95

    Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
                100             105

(2) INFORMATION FOR SEQ ID NO:84:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

    Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
    1               5               10              15

    Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala
                20              25              30

    Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Ala
            35              40              45

```
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50                  55                  60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65                  70                  75                  80

Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Arg Thr Phe
                85                  90                  95

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
              100                 105
```

(2) INFORMATION FOR SEQ ID NO:85:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 106 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1               5               10                  15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala
            20                  25                  30

Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Ala
        35                  40                  45

Ala Ser Thr Leu Gln Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly
    50                  55                  60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65                  70                  75                  80

Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro His Thr Phe
                85                  90                  95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
              100                 105
```

(2) INFORMATION FOR SEQ ID NO:86:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
1               5               10              15

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ile Ser Asn Tyr Leu
        20              25              30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
        35              40              45

Gly Val Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50              55              60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65              70              75              80

Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Thr Ser Pro Trp Thr
            85              90              95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100             105

(2) INFORMATION FOR SEQ ID NO:87:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
1               5               10              15

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asn Tyr Leu
        20              25              30

Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
        35              40              45

Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50              55              60

```
Gly Ser Gly Thr Ala Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65                  70              75                  80

Asp Val Ala Ile Tyr Tyr Cys Gln Gln Tyr His Ser Ser Pro Tyr Thr
                85                  90                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100             105
```

(2) INFORMATION FOR SEQ ID NO:88:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 108 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
1               5               10              15

Ala Thr Leu Ser Cys Arg Ala Ser His Arg Val Asn Asn Asn Phe Leu
            20              25              30

Ala Trp Tyr Gln Gln Lys Pro Gln Ala Pro Arg Leu Leu Ile Ser Gly
        35              40              45

Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
    50              55              60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Asp Asp
65                  70              75                  80

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Ser Pro Leu Tyr Ser
                85                  90                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100             105
```

(2) INFORMATION FOR SEQ ID NO:89:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 105 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
Glu Leu Thr Gln Ser Pro Ala Ser Val Ser Ala Ser Val Gly Asp Thr
1               5               10              15
```

```
Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile His Asn Trp Leu Ala
            20              25              30
```

```
Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
        35              40              45
```

```
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly
    50              55              60
```

```
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65              70              75              80
```

```
Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Ser Phe Pro Lys Phe Gly
            85              90              95
```

```
Pro Gly Thr Val Val Asp Ile Lys Arg
        100             105
```

(2) INFORMATION FOR SEQ ID NO:90:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 107 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
1               5               10              15
```

```
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Asn Asn Tyr Leu
            20              25              30
```

```
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
        35              40              45
```

```
Gly Ser Ser Thr Arg Gly Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly
    50              55              60
```

```
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65              70              75              80
```

```
      Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Gly Asn Ser Val Tyr Thr
                      85              90                  95

      Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
                  100              105
```

(2) INFORMATION FOR SEQ ID NO:91:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 104 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
      Gln Ser Pro Asp Thr Leu Ser Leu Asn Pro Gly Glu Arg Ala Thr Leu
      1               5               10                  15

      Ser Cys Arg Ala Ser His Arg Ile Ser Ser Lys Arg Leu Ala Trp Tyr
                  20              25                  30

      Gln His Lys Arg Gly Gln Ala Pro Arg Leu Leu Ile Tyr Val Cys Pro
                  35              40              45

      Asn Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
          50              55              60

      Thr Asp Phe Thr Leu Thr Tyr Ser Arg Leu Glu Pro Glu Asp Phe Ala
      65              70              75                  80

      Met Tyr Tyr Cys Gln Tyr Tyr Gly Gly Ser Ser Tyr Thr Phe Gly Gln
                  85              90                  95

      Gly Thr Lys Val Glu Ile Thr Arg
                  100
```

(2) INFORMATION FOR SEQ ID NO:92:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 104 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
Gln Ser Pro Ser His Leu Ser Leu Ser Pro Gly Glu Arg Ala Ile Leu
1               5               10              15

Ser Cys Arg Ala Ser Gln Arg Val Ser Ala Pro Tyr Leu Ala Trp Tyr
            20              25              30

Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Gly Ala Ser
            35              40              45

Thr Arg Ala Thr Asp Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
    50              55              60

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
65              70              75              80

Ile Tyr Tyr Cys Gln Val Tyr Gly Gln Ser Pro Val Leu Phe Gly Gln
            85              90              95

Gly Thr Lys Leu Glu Met Lys Arg
            100
```

(2) INFORMATION FOR SEQ ID NO:93:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 105 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Asp Arg Ala Thr Leu
1               5               10              15

Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Ser Phe Leu Ala Trp Tyr
            20              25              30

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Ala Ser
            35              40              45

Met Arg Ala Thr Gly Ile Pro Asp Arg Phe Arg Gly Ser Val Ser Gly
    50              55              60

Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala
65              70              75              80

Val Tyr Tyr Cys Gln Arg Phe Gly Thr Ser Pro Leu Tyr Thr Phe Gly
            85              90              95
```

```
           Gln Gly Thr Lys Leu Glu Met Lys Arg
                       100             105
```

(2) INFORMATION FOR SEQ ID NO:94:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 104 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
1               5               10              15

Ser Cys Arg Ala Ser Gln Ser Phe Ser Ser Asn Phe Leu Ala Trp Tyr
            20              25              30

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Val His Pro
        35              40              45

Asn Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
    50              55              60

Thr Asp Phe Thr Leu Thr Ile Arg Arg Leu Glu Pro Glu Asp Phe Ala
65              70              75              80

Val Tyr Tyr Cys Gln Gln Tyr Gly Ala Ser Leu Val Ser Phe Gly Pro
            85              90              95

Gly Thr Lys Val His Ile Lys Arg
            100
```

(2) INFORMATION FOR SEQ ID NO:95:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
1               5               10              15
```

```
Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile Arg Ser Arg Arg Val
            20              25            30

Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His
        35              40              45

Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser
    50              55              60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Val Glu Pro Glu
65              70              75              80

Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr
                85              90              95

Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys Arg Thr
            100             105
```

(2) INFORMATION FOR SEQ ID NO:96:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Thr Pro Gly Glu Arg
1               5               10              15

Ala Thr Leu Ser Cys Arg Thr Ser His Ser Ile Arg Ser Arg Arg Leu
            20              25              30

Ala Trp Tyr Gln Val Lys Gly Gly Gln Ala Pro Arg Leu Leu Ile Tyr
        35              40              45

Gly Val Ser Asn Arg Ala Gly Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50              55              60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65              70              75              80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Arg Tyr Thr
                85              90              95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100             105
```

(2) INFORMATION FOR SEQ ID NO:97:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
Glu Leu Thr Gln Ala Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
1               5               10              15

Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile Arg Ser Arg Arg Val
            20              25              30

Arg Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His
        35              40              45

Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser
    50              55              60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Val Glu Pro Glu
65              70              75              80

Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr
            85              90              95

Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys Arg
        100             105
```

(2) INFORMATION FOR SEQ ID NO:98:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```
Glu Leu Thr Gln Ala Pro Gly Thr Leu Ser Leu Ser Pro Gly Asp Arg
1               5               10              15

Ala Thr Phe Ser Cys Arg Ser Ser His Asn Ile Arg Ser Arg Arg Val
            20              25              30
```

```
    Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His
                35              40          45

    Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser
        50              55                  60

    Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu
    65              70                  75                  80

    Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr
                85                  90                  95

    Phe Gly Gln Gly Thr Lys Leu Asp Phe Lys Arg Thr
                100             105
```

(2) INFORMATION FOR SEQ ID NO:99:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```
    Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    1               5                   10                  15

    Ala Thr Leu Ser Cys Arg Ala Gly Gln Ser Ile Ser Ser Asn Tyr Leu
                20                  25                  30

    Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                35              40                  45

    Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
        50              55                  60

    Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Arg Leu Glu Pro Glu
    65              70                  75                  80

    Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Thr Ser Pro Tyr Thr
                85                  90                  95

    Phe Gly Gln Gly Thr Gln Leu Asp Ile Lys Arg Thr
                100             105
```

(2) INFORMATION FOR SEQ ID NO:100:

    (i) SEQUENCE CHARACTERISTICS:

     (A) LENGTH: 104 amino acids
     (B) TYPE: amino acid
     (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: protein


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```
Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
1               5               10              15

Ser Cys Arg Ala Ser Gln Ser Leu Ser Asn Asn Tyr Leu Ala Trp Tyr
            20              25              30

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser
            35              40              45

Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly
            50              55              60

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
65              70              75              80

Val Tyr Tyr Cys Gln Gln Tyr Gly Asn Ser Val Tyr Thr Phe Gly Gln
                85              90              95

Gly Thr Lys Leu Glu Ile Lys Arg
                100
```

(2) INFORMATION FOR SEQ ID NO:101:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 106 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: protein


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5               10              15

Val Thr Ile Thr Cys Arg Thr Ser Gln Gly Ile Ser Asn Tyr Leu Ala
            20              25              30

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Gly
            35              40              45
```

```
        Ala Ser Thr Leu Gln Ser Gly Gly Pro Ser Arg Phe Ser Gly Ser Gly
            50                  55                  60

        Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
        65                  70                  75                  80

        Val Ala Thr Tyr Ser Cys Gln Asn Tyr Asp Ser Ala Pro Trp Thr Phe
                        85                  90                  95

        Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
                        100                 105
```

(2) INFORMATION FOR SEQ ID NO:102:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
    Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
    1                   5                   10                  15

    Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Asn
                    20                  25                  30

    Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
                35                  40                  45

    Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        50                  55                  60

    Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Leu Gln Pro Glu Asp
    65                  70                  75                  80

    Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Pro Leu Thr
                    85                  90                  95

    Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
                    100                 105
```

(2) INFORMATION FOR SEQ ID NO:103:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5               10              15

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Asn Tyr Leu Asn
            20              25              30

Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile His Thr
        35              40              45

Ala Phe Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Thr Ala
    50              55              60

Ser Gly Thr Glu Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp
65              70              75              80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe
            85              90              95

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100             105
```

(2) INFORMATION FOR SEQ ID NO:104:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5               10              15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
            20              25              30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
        35              40              45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50              55              60
```

```
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65              70              75                  80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe
            85                  90                  95

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:105:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 107 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5               10                  15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
            20                  25                  30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
        35                  40                  45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        50                  55                  60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65              70              75                  80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Gln Thr Phe
            85                  90                  95

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:106:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 104 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
1               5                   10                  15

Thr Cys Arg Ala Ser Gln Thr Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
            20              25              30

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
        35              40              45

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr
    50              55              60

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
65              70              75              80

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly
            85              90              95

Thr Lys Leu Glu Ile Lys Arg Thr
            100

(2) INFORMATION FOR SEQ ID NO:107:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5                   10                  15

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn
            20              25              30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
        35              40              45

Ala Ser Asn Ser Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50              55              60

Ser Gly Arg Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp
65              70              75              80

```
Val Ala Thr Tyr Tyr Cys Gln Gln His Gln Asn Val Pro Leu Thr Phe
            85                  90                  95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
        100                 105
```

(2) INFORMATION FOR SEQ ID NO:108:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 107 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5                   10                  15

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn His Leu Asn
            20                  25                  30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
        35                  40                  45

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50                  55                  60

Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp
65                  70                  75                  80

Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu Thr Phe
            85                  90                  95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
        100                 105
```

(2) INFORMATION FOR SEQ ID NO:109:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 108 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```
Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5               10              15

Ile Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Asn Asn Tyr Leu Asn
            20              25              30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
        35              40              45

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50              55              60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65              70              75              80

Phe Ala Thr Tyr Phe Cys Gln Gln Ser Tyr Asn Thr Pro Pro Trp Thr
            85              90              95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
        100             105
```

(2) INFORMATION FOR SEQ ID NO:110:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 108 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
1               5               10              15

Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Ser Asn Tyr Leu
            20              25              30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Thr Pro Arg Val Val Ile Tyr
        35              40              45

Ser Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
    50              55              60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65              70              75              80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Asp Ala Gln Tyr Thr
            85              90              95
```

```
        Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
                 100                 105
```

(2) INFORMATION FOR SEQ ID NO:111:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 93 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Ser Asn
1               5               10              15

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Thr Pro Arg Val Val
             20              25              30

Ile Tyr Ser Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser
         35              40              45

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
     50              55              60

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Asp Ala Gln
65              70              75              80

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
             85              90
```

(2) INFORMATION FOR SEQ ID NO:112:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 104 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Thr Val Thr
1               5               10              15

Phe Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr
             20              25              30
```

```
    His Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Ser Asp Ala Ser
            35              40              45

    Asp Leu Glu Ile Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Ala
        50              55              60

    Thr Tyr Phe Ser Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Gly
    65              70              75              80

    Thr Tyr Tyr Cys Gln Gln Tyr Ala Asp Leu Ile Thr Phe Gly Gly Gly
                85              90              95

    Thr Lys Val Glu Ile Lys Arg Thr
                100
```

(2) INFORMATION FOR SEQ ID NO:113:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 96 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
    Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
    1               5               10              15

    Gly Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
            20              25              30

    Leu Leu Ile Phe Asp Ala Ser Thr Arg Asp Thr Tyr Ile Pro Asp Thr
            35              40              45

    Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ala Leu Thr Ile Ser Ser
        50              55              60

    Leu Gln Ser Glu Asp Phe Gly Phe Tyr Tyr Cys Gln Gln Tyr Asp Asn
    65              70              75              80

    Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Val Lys Arg Thr
                85              90              95
```

(2) INFORMATION FOR SEQ ID NO:114:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

    Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Asp Arg
    1               5                   10                  15

    Ala Thr Phe Ser Cys Arg Ser Ser His Asn Ile Arg Ser Arg Arg Val
                20                  25                  30

    Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His
            35                  40                  45

    Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser Gly Ser
        50                  55                  60

    Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu
    65                  70                  75                  80

    Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr
                    85                  90                  95

    Phe Gly Gln Gly Thr Lys Leu Asp Phe Lys Arg
                    100                 105

(2) INFORMATION FOR SEQ ID NO:115:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

    Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    1               5                   10                  15

    Ala Thr Phe Ser Cys Arg Ser Ser His Asn Ile Arg Ser Arg Arg Val
                20                  25                  30

    Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His
            35                  40                  45

    Gly Val Ser Asn Arg Ala Thr Gly Ile Ser Asp Arg Phe Ser Gly Ser

                50                      55                      60

        Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu
        65                      70                      75                      80

        Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser Tyr Thr
                        85                      90                      95

        Phe Gly Gln Gly Thr Lys Leu Asp Phe Lys Arg
                        100                     105

(2) INFORMATION FOR SEQ ID NO:116:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

        Glu Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Asn Val Gly Glu Arg
        1                   5                   10                      15

        Ala Thr Leu Ser Cys Arg Ala Ser His Arg Ile Ser Ser Arg Arg Leu
                        20                      25                      30

        Ala Trp Tyr Gln His Lys Arg Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                        35                      40                      45

        Gly Val Ser Ser Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser
                50                      55                      60

        Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Arg Leu Glu Pro Glu
        65                      70                      75                      80

        Asp Phe Ala Met Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Thr
                        85                      90                      95

        Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
                        100                     105

(2) INFORMATION FOR SEQ ID NO:117:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

    Glu Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Asn Ala Gly Glu Arg
    1               5               10              15

    Ala Thr Leu Ser Cys Arg Ala Ser His Arg Ile Ser Ser Arg Arg Leu
                20              25              30

    Ala Trp Tyr Gln His Lys Arg Gly Gln Ala Pro Arg Leu Leu Ile Tyr
            35              40              45

    Gly Val Ser Asn Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser
        50              55              60

    Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Arg Leu Glu Pro Glu
    65              70              75              80

    Asp Phe Ala Ile Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Thr
                85              90              95

    Phe Gly Gln Gly Thr Thr Val Asp Ile Lys Arg
                100             105

(2) INFORMATION FOR SEQ ID NO:118:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

    Glu Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Asn Thr Gly Glu Arg
    1               5               10              15

    Ala Thr Leu Ser Cys Arg Ala Ser His Arg Ile Gly Ser Arg Arg Leu
                20              25              30

    Ala Trp Tyr Gln His Arg Arg Gly Gln Ala Pro Arg Leu Leu Ile Tyr
            35              40              45

    Gly Val Ser Asn Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser
        50              55              60

```
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65              70              75                      80

Asp Phe Ala Ile Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Thr
                85              90                  95

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
            100             105
```

(2) INFORMATION FOR SEQ ID NO:119:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Thr Pro Gly Glu Arg
1               5               10              15

Ala Ile Leu Ser Cys Lys Thr Ser His Asn Ile Trp Ser Arg Arg Leu
                20              25              30

Ala Trp Tyr Gln Leu Lys Ser Gly Gln Ala Pro Arg Leu Leu Ile Tyr
            35              40              45

Gly Val Ser Lys Arg Ala Gly Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50              55              60

Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Arg Val Glu Pro Glu
65              70              75                      80

Asp Phe Ala Val Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ala Tyr Thr
                85              90                  95

Phe Gly Gln Gly Thr Lys Leu Asp Ile Lys Arg
            100             105
```

(2) INFORMATION FOR SEQ ID NO:120:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Thr Pro Gly Glu Arg
1               5                   10                  15

Ala Ile Leu Ser Cys Lys Thr Ser His Asn Ile Trp Ser Arg Arg Leu
              20                  25                  30

Ala Trp Tyr Gln Leu Lys Ser Gly Gln Ala Pro Arg Leu Leu Ile Tyr
          35                  40                  45

Gly Val Ser Lys Arg Ala Gly Gly Ile Pro Asp Arg Phe Ser Gly Ser
      50                  55                  60

Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Arg Val Glu Pro Glu
65                  70                  75                  80

Asp Phe Ala Val Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ala Tyr Thr
              85                  90                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
              100                 105

(2) INFORMATION FOR SEQ ID NO:121:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Ser Thr Pro Gly Glu Arg
1               5                   10                  15

Ala Ile Leu Ser Cys Lys Thr Ser His Asn Ile Trp Ser Arg Arg Leu
              20                  25                  30

Ala Trp Tyr Gln Val Lys Ser Gly Leu Pro Pro Arg Leu Leu Ile His
          35                  40                  45

Gly Val Ser Arg Arg Ala Gly Gly Ile Pro Asp Arg Phe Ser Gly Ser
      50                  55                  60

Gly Ser Ala Arg Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Ala
65                  70                  75                  80

Asp Phe Ala Val Tyr Tyr Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Ser
                85                      90                95

Phe Gly Gln Gly Thr Lys Leu Asp Phe Asn Arg
              100                 105

(2) INFORMATION FOR SEQ ID NO:122:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

    Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Asn Pro Gly Glu Arg
    1               5               10              15

    Ala Val Leu Ser Cys Arg Thr Ser Arg Asn Ile Trp Ser Arg Arg Leu
                20              25              30

    Ala Trp Tyr Gln Val Arg Arg Gly Gln Ala Pro Arg Leu Leu Ile His
            35              40              45

    Gly Val Ser Lys Arg Ala Gly Gly Val Pro Asp Arg Phe Ser Gly Ser
        50              55              60

    Gly Ser Ala Arg Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
    65              70              75              80

    Asp Phe Ala Val Tyr Phe Cys Gln Thr Tyr Gly Gly Ser Ser Tyr Thr
                85              90              95

    Phe Gly Gln Gly Asn Lys Leu Asp Ile Arg Arg
              100                 105

(2) INFORMATION FOR SEQ ID NO:123:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 126 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5               10              15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20              25              30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp
        35              40              45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Pro Pro Lys
        50              55              60

Phe Gln Asp Arg Val Ser Leu Thr Arg Asp Thr Ser Ala Gly Thr Val
65              70              75              80

Tyr Leu Glu Leu Thr Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr
            85              90              95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn
        100             105             110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
        115             120             125

(2) INFORMATION FOR SEQ ID NO:124:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5               10              15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20              25              30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp
        35              40              45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys
        50              55              60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val
65              70              75              80

```
Tyr Leu Glu Leu Arg Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr
            85                  90                  95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn
            100                 105                 110

Tyr Tyr Met Asp Val Trp Gly Arg Gly Thr Thr Val Thr
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:125:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5               10                  15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20              25                  30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp
            35              40                  45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys
        50                  55                  60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val
65                  70                  75                  80

Tyr Leu Glu Leu Arg Ser Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr
            85                  90                  95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn
            100                 105                 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:126:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5                   10              15

Ala Ser Val Lys Ile Ser Cys Gln Ala Ser Gly Tyr Arg Phe Thr Asn
            20              25              30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly Gln Arg Pro Glu Trp
        35              40              45

Met Gly Trp Phe Asn Pro Ala Asn Gly Ile Lys Glu Ile Ser Pro Lys
        50              55              60

Phe Gln Asp Arg Val Ser Phe Thr Gly Asp Thr Ser Ala Ser Thr Ala
65              70              75              80

Tyr Val Glu Leu Arg Asn Leu Arg Ser Ala Asp Thr Ala Val Tyr Tyr
            85              90              95

Cys Ala Arg Val Gly Pro Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn
            100             105             110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
        115             120

(2) INFORMATION FOR SEQ ID NO:127:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5                   10              15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20              25              30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp
        35              40              45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys
    50                      55                  60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val
65                      70                  75                  80

Tyr Leu Glu Leu Arg Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Phe Pro Gln Asp Asn
            100                 105                 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
        115                 120

(2) INFORMATION FOR SEQ ID NO:128:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5               10                  15

Ala Ser Val Lys Leu Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20                  25                  30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp
            35                  40                  45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Ser Pro Lys
    50                      55                  60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val
65                      70                  75                  80

Tyr Leu Glu Leu Arg Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn
            100                 105                 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr
        115                 120                 125

(2) INFORMATION FOR SEQ ID NO:129:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Gln Val Lys Leu Leu Glu Gln Ser Gly Thr Glu Val Lys Lys Pro Gly
1               5               10              15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Arg Phe Thr Asn
        20              25              30

Phe Pro Leu His Trp Val Arg Gln Ala Pro Gly Gln Arg Pro Glu Trp
        35              40              45

Met Gly Trp Ile Lys Ile Val Asn Gly Glu Lys Lys Tyr Ser Gln Lys
        50              55              60

Phe Val Asp Arg Val Thr Phe Thr Gly Asp Thr Ser Ala Asn Thr Ala
65              70              75              80

Tyr Met Glu Val Arg Gly Leu Arg Ser Ala Asp Thr Ala Thr Tyr Tyr
                85              90              95

Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Met Asp Pro Gln Ala Asn
            100             105             110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr
        115             120             125

(2) INFORMATION FOR SEQ ID NO:130:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5               10              15

```
Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20              25              30

Phe Val Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Phe Glu Trp
            35              40              45

Met Gly Trp Ile Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser Ala Lys
    50              55              60

Phe Arg Asp Arg Val Thr Phe Thr Ala Asp Thr Asp Ala Asn Thr Ala
65              70              75              80

Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala Asp Thr Ala Ile Tyr Tyr
                85              90              95

Cys Ala Arg Val Gly Pro Tyr Thr Trp Asp Asp Ser Pro Gln Asp Asn
            100             105             110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
    115             120
```

(2) INFORMATION FOR SEQ ID NO:131:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5               10              15

Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20              25              30

Phe Val Leu His Trp Ala Arg Gln Ala Pro Thr Gln Asp Leu Glu Trp
            35              40              45

Met Gly Trp Ile Asn Pro Ala Asn Gly Val Lys Glu Ile Ser Pro Lys
    50              55              60

Phe Gln Asp Arg Val Ser Leu Thr Gly Asp Thr Ser Ala Ser Thr Val
65              70              75              80

Tyr Leu Glu Leu Arg Ser Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr
                85              90              95
```

```
Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn
            100                 105             110
```

```
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
            115             120
```

(2) INFORMATION FOR SEQ ID NO:132:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 124 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
Gln Val Lys Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1               5               10              15
```

```
Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe Ser Asn
            20              25              30
```

```
Phe Val Leu His Trp Ala Arg Gln Ala Pro Gly His Arg Pro Glu Trp
            35              40              45
```

```
Met Gly Trp Ile Asn Pro Ala Asn Gly Val Thr Glu Ile Pro Pro Lys
        50              55              60
```

```
Phe Gln Asp Arg Val Ser Leu Thr Arg Asp Thr Ser Ala Gly Thr Val
65              70              75              80
```

```
Tyr Leu Glu Leu Thr Asn Leu Arg Phe Ala Asp Thr Ala Val Tyr Tyr
            85              90              95
```

```
Cys Ala Arg Val Gly Glu Trp Thr Trp Asp Asp Ser Pro Gln Asp Asn
            100             105             110
```

```
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
            115             120
```

(2) INFORMATION FOR SEQ ID NO:133:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TCGAGGGTCG GTCGGTCTCT AGACGGTCGG TCGGTCA                              37

(2) INFORMATION FOR SEQ ID NO:134:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 37 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTAGTGACCG ACCGACCGTC TAGAGACCGA CCGACCC                              37

(2) INFORMATION FOR SEQ ID NO:135:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 32 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CGGTCGGTCG GTCCTCGAGG GTCGGTCGGT CT                                   32

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 40 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTAGAGACCG ACCGACCCTC GAGGACCGAC CGACCGAGCT                                    40

(2) INFORMATION FOR SEQ ID NO:137:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAAGGAGACA GGATCCATGA AATAC                                                    25

(2) INFORMATION FOR SEQ ID NO:138:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

AGGGCGAATT GGATCCCGGG CCCCC                                          25

(2) INFORMATION FOR SEQ ID NO:139:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 29 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTAGTCATCA TCATCATCAT TAAGCTAGC                                      29

(2) INFORMATION FOR SEQ ID NO:140:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 29 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTAGGCTAGC TTAATGATGA TGATGATGA                                      29

(2) INFORMATION FOR SEQ ID NO:141:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 13 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: peptide

         (v) FRAGMENT TYPE: internal


        (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 1
             (D) OTHER INFORMATION: /label= J

        (ix) FEATURE:
             (A) NAME/KEY: Modified-site
             (B) LOCATION: 13
             (D) OTHER INFORMATION: /label= ZC


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

        Ser Ile Ser Ile Gly Pro Gly Arg Ala Phe Tyr Thr Gly
        1               5                   10

(2) INFORMATION FOR SEQ ID NO:142:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 126 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

        Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser
        1               5                   10                  15

        Leu Thr Cys Thr Val Ser Gly Gly Ser Leu Ser Ser Phe Asp Trp Asn
                    20                  25                  30

        Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly Arg Ile
                    35                  40                  45

        Tyr Pro Ser Gly Asn Thr His Tyr Asn Pro Ser Leu Arg Ser Arg Val
                50                  55                  60

        Thr Met Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser Val Lys Leu Thr
        65                  70                  75                  80

        Ser Val Thr Ala Ala Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Glu Asn
                        85                  90                  95

```
Thr Gly Arg Thr Ile Glu Glu Ile Gly Asn Phe Phe Asp Ile Trp Gly
            100                 105             110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
            115                 120             125
```

(2) INFORMATION FOR SEQ ID NO:143:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 122 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
Leu Leu Lys Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5               10              15

Leu Ser Cys Val Ile Ser Ala Phe Ser Phe Ser Gly Tyr Asn Ile Asn
            20              25              30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
            35              40              45

Ser Met Ser Thr Gly Ser Leu Ser Tyr Ala Asp Ser Met Lys Gly Arg
    50              55              60

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Glu Met
65              70              75              80

Ser Ser Leu Thr Ala Glu Asp Thr Ala Met Tyr Tyr Cys Ala Ala Arg
            85              90              95

Thr Pro Leu Val Gly Arg Ala Leu Asp Ile Trp Gly Gln Gly Thr Val
            100             105             110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly
            115             120
```

(2) INFORMATION FOR SEQ ID NO:144:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 132 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg
1               5               10              15

Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met Asn
            20              25              30

Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val Ala Tyr Ile
        35              40              45

Ser Ser Ser Arg Lys Tyr Thr Glu Tyr Ala Asp Ser Val Lys Gly Arg
    50              55              60

Phe Thr Ile Ser Arg Glu Asn Ala Lys Tyr Ser Val Phe Leu Gln Leu
65              70              75              80

Asp Ser Leu Thr Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Gly
            85              90              95

Arg Asp Phe Tyr Ser Gly Phe Gly Arg Arg Asp Asp Phe His Leu His
            100             105             110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala
        115             120             125

Ser Thr Lys Gly
    130
```

(2) INFORMATION FOR SEQ ID NO:145:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 126 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
Leu Leu Glu Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
1               5               10              15

Arg Ile Ser Cys Val Ala Ser Gly Asp Ile Phe Tyr Ser Tyr Ala Met
            20              25              30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ser
        35              40              45
```

```
Ile Ser Gly Thr Gly Gly Ser Asn Tyr Tyr Ala Asp Ser Val Lys Gly
    50                  55              60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Tyr Leu Gln
65                  70              75                  80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg
            85              90                  95

Asp Arg Gly Pro Arg Ile Gly Ile Arg Gly Trp Phe Asp Ser Trp Gly
            100             105             110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
            115             120             125
```

(2) INFORMATION FOR SEQ ID NO:146:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 124 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
1               5               10                  15

Leu Ser Cys Ala Ala Ser Gly Phe Leu Tyr Ser Ser Phe Ala Met Ser
            20              25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Ala Trp Val Ser Thr Ile
            35              40                  45

Ser Ala Ser Gly Gly Ser Thr Lys Tyr Ala Asp Ser Val Lys Gly Arg
    50                  55              60

Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Ile Tyr Leu Gln Met
65                  70              75                  80

Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asn
            85              90                  95

Phe Arg Ala Phe Ala Arg Asp Pro Trp Gly Asp Trp Gly Gln Gly Thr
            100             105             110

Leu Val Thr Val Ser Ser Ala Ser Ala Ser Thr Lys
            115             120
```

(2) INFORMATION FOR SEQ ID NO:147:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 109 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
Met Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5               10              15

Glu Arg Val Ile Val Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20              25              30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35              40              45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
        50              55              60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65              70              75              80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Gly
            85              90              95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
        100             105
```

(2) INFORMATION FOR SEQ ID NO:148:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 112 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
Met Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5               10              15

Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser His Ser Ile His Thr Arg
            20              25              30
```

        Arg Val Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val
            35              40              45

        Ile His Gly Val Ser Asn Arg Ala Ser Gly Ile Ser Asp Arg Phe Ser
            50              55              60

        Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Val Glu
        65              70              75              80

        Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr Gly Ala Ser Ser
                    85              90              95

        Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys Arg Thr Val Val
                    100             105             110


(2) INFORMATION FOR SEQ ID NO:149:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

    Met Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
    1               5               10              15

    Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Gly
                20              25              30

    Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
            35              40              45

    Ile Tyr Gly Ala Ser Thr Arg Ala Thr Asp Ile Pro Asp Arg Phe Ser
        50              55              60

    Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Ala Ile Ser Arg Leu Glu
    65              70              75              80

    Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Gly Ser His
                85              90              95

    Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
                100             105             110

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 111 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Ala Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5               10              15

Asp Arg Val Thr Ile Thr Cys Arg Pro Ser Gln Gly Ile Gly Arg Phe
            20              25              30

Phe Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35              40              45

Tyr Ala Ala Asp Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50              55              60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65              70              75              80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
            85              90              95

Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys Arg Thr Val Ala
            100             105             110

(2) INFORMATION FOR SEQ ID NO:151:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 112 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Met Ala Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5               10              15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Ser Ser Ser
            20              25              30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Val

```
                35                    40                    45
```

    Ile Phe Gly Ala Tyr Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
        50                    55                    60

    Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
        65                    70                    75                    80

    Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                    85                    90                    95

    Ile Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
                    100                   105                   110


(2) INFORMATION FOR SEQ ID NO:152:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 729 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)


    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 9..715


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
AGCTTACC ATG GGT GTG CCC ACT CAG GTC CTG GGG TTG CTG CTG CTG TGG          50
         Met Gly Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp
          1               5                   10

CTT ACA GAT GCC AGA TGT GAG ATC GTT CTC ACG CAG TCT CCA GGC ACC          98
Leu Thr Asp Ala Arg Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
 15                  20                  25                  30

CTG TCT CTG TCT CCA GGG GAA AGA GCC ACC TTC TCC TGT AGG TCC AGT          146
Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser
                35                  40                  45

CAC AGC ATT CGC AGC CGC CGC GTA GCC TGG TAC CAG CAC AAA CCT GGC          194
His Ser Ile Arg Ser Arg Arg Val Ala Trp Tyr Gln His Lys Pro Gly
                50                  55                  60

CAG GCT CCA AGG CTG GTC ATA CAT GGT GTT TCC AAT AGG GCC TCT GGC          242
Gln Ala Pro Arg Leu Val Ile His Gly Val Ser Asn Arg Ala Ser Gly
                65                  70                  75
```

```
ATC TCA GAC AGG TTC AGC GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC       290
Ile Ser Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    80                      85                  90

ACC ATC ACC AGA GTG GAG CCT GAA GAC TTT GCA CTG TAC TAC TGT CAG       338
Thr Ile Thr Arg Val Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln
95                      100                 105                 110

GTC TAT GGT GCC TCC TCG TAC ACT TTT GGC CAG GGG ACC AAA CTG GAG       386
Val Tyr Gly Ala Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu
                115                 120                 125

AGG AAA CGA ACT GTG CCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT       434
Arg Lys Arg Thr Val Pro Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
            130                 135                 140

GAT GAG CAG TTG AAA TCT GGG ACT GCC TCT GTT GTG TGC CTG CTG AAT       482
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
        145                 150                 155

AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC       530
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
    160                 165                 170

CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG       578
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
175                 180                 185                 190

GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC       626
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
                195                 200                 205

TAC GAG AAA CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG       674
Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
            210                 215                 220

AGT TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TA ATTCTAGAGA     725
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
        225                 230                 235

ATTC                                                                  729
```

(2) INFORMATION FOR SEQ ID NO:153:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 235 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
Met Gly Val Pro Thr Gln Val Leu Gly Leu Leu Leu Trp Leu Thr
1               5               10              15

Asp Ala Arg Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
            20              25              30

Leu Ser Pro Gly Glu Arg Ala Thr Phe Ser Cys Arg Ser Ser His Ser
        35              40              45

Ile Arg Ser Arg Arg Val Ala Trp Tyr Gln His Lys Pro Gly Gln Ala
    50              55              60

Pro Arg Leu Val Ile His Gly Val Ser Asn Arg Ala Ser Gly Ile Ser
65              70              75              80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
            85              90              95

Thr Arg Val Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Val Tyr
        100             105             110

Gly Ala Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Arg Lys
        115             120             125

Arg Thr Val Pro Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130             135             140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145             150             155             160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
            165             170             175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180             185             190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195             200             205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210             215             220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225             230             235
```

(2) INFORMATION FOR SEQ ID NO:154:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3282 base pairs
        (B) TYPE: nucleic acid

```
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)


     (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 15..452



     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:


AATTCGCCGC CACC ATG GAA TGG AGC TGG GTC TTT CTC TTC TTC CTG TCA       50
              Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser
               1               5                  10


GTA ACT ACA GGT GTC CAC TCC CAG GTT CAG CTG GTT CAG TCC GGG GCT       98
Val Thr Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala
         15              20              25


GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTT TCT TGT CAG GCT TCT      146
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Gln Ala Ser
     30              35              40


GGA TAC AGA TTC AGT AAC TTT GTT ATT CAT TGG GTG CGC CAG GCC CCC      194
Gly Tyr Arg Phe Ser Asn Phe Val Ile His Trp Val Arg Gln Ala Pro
 45              50              55              60


GGA CAG AGG TTT GAG TGG ATG GGA TGG ATC AAT CCT TAC AAC GGA AAC      242
Gly Gln Arg Phe Glu Trp Met Gly Trp Ile Asn Pro Tyr Asn Gly Asn
             65              70              75


AAA GAA TTT TCA GCG AAG TTC CAG GAC AGA GTC ACC TTT ACC GCG GAC      290
Lys Glu Phe Ser Ala Lys Phe Gln Asp Arg Val Thr Phe Thr Ala Asp
             80              85              90


ACA TCC GCG AAC ACA GCC TAC ATG GAG TTG AGG AGC CTC AGG TCT GCA      338
Thr Ser Ala Asn Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala
         95              100             105


GAC ACG GCT GTT TAT TAT TGT GCG AGA GTG GGG CCA TAT AGT TGG GAT      386
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val Gly Pro Tyr Ser Trp Asp
     110             115             120


GAT TCT CCC CAG GAC AAT TAT TAT ATG GAC GTC TGG GGC AAA GGA ACC      434
Asp Ser Pro Gln Asp Asn Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr
 125             130             135             140


ACG GTC ATC GTG AGC TCA GCTTCCACCA AGGGCCCATC GGTCTTCCCC            482
Thr Val Ile Val Ser Ser
```

145

CTGGCACCCT CCTCCAAGAG CACCTCTGGG GGCACAGCGG CCCTGGGCTG CCTGGTCAAG    542

GACTACTTCC CCGAACCGGT GACGGTGTCG TGGAACTCAG GCGCCCTGAC CAGCGGCGTG    602

CACACCTTCC CGGCTGTCCT ACAGTCCTCA GGACTCTACT CCCTCAGCAG CGTGGTGACC    662

GTGCCCTCCA GCAGCTTGGG CACCCAGACC TACATCTGCA ACGTGAATCA CAAGCCCAGC    722

AACACCAAGG TGGACAAGAA AGTTGGTGAG AGGCCAGCAC AGGGAGGGAG GGTGTCTGCT    782

GGAAGCCAGG CTCAGCGCTC CTGCCTGGAC GCATCCCGGC TATGCAGCCC CAGTCCAGGG    842

CAGCAAGGCA GGCCCCGTCT GCCTCTTCAC CCGGAGGCCT CTGCCCGCCC CACTCATGCT    902

CAGGGAGAGG GTCTTCTGGC TTTTTCCCCA GGCTCTGGGC AGGCACAGGC TAGGTGCCCC    962

TAACCCAGGC CCTGCACACA AAGGGGCAGG TGCTGGGCTC AGACCTGCCA AGAGCCATAT   1022

CCGGGAGGAC CCTGCCCCTG ACCTAAGCCC ACCCCAAAGG CCAAACTCTC CACTCCCTCA   1082

GCTCGGACAC CTTCTCTCCT CCCAGATTCG AGTAACTCCC AATCTTCTCT CTGCAGAGCC   1142

CAAATCTTGT GACAAAACTC ACACATGCCC ACCGTGCCCA GGTAAGCCAG CCCAGGCCTC   1202

GCCCTCCAGC TCAAGGCGGG ACAGGTGCCC TAGAGTAGCC TGCATCCAGG GACAGGCCCC   1262

AGCCGGGTGC TGACACGTCC ACCTCCATCT CTCCCTCAGC ACCTGAGGCC GCGGGAGGAC   1322

CATCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCCT CATGATCTCC CGGACCCCTG   1382

AGGTCACATG CGTGGTGGTG GACGTGAGCC ACGAAGACCC TGAGGTCAAG TTCAACTGGT   1442

ACGTGGACGG CGTGGAGGTG CATAATGCCA AGACAAAGCC GCGGGAGGAG CAGTACAACA   1502

GCACGTACCG TGTGGTCAGC GTCCTCACCG TCCTGCACCA GGACTGGCTG AATGGCAAGG   1562

AGTACAAGTG CAAGGTCTCC AACAAAGCCC TCCCAGCCCC CATCGAGAAA ACCATCTCCA   1622

AAGCCAAAGG TGGGACCCGT GGGGTGCGAG GCCACATGG ACAGAGGCCG GCTCGGCCCA   1682

CCCTCTGCCC TGAGAGTGAC CGCTGTACCA ACCTCTGTCC CTACAGGGCA GCCCCGAGAA   1742

CCACAGGTGT ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTCAGCCTG   1802

ACCTGCCTGG TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG   1862

CAGCCGGAGA ACAACTACAA GACCACGCCT CCCGTGCTGG ACTCCGACGG CTCCTTCTTC   1922

CTCTACAGCA AGCTCACCGT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC   1982

TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG    2042

GGTAAATGAG TGCGACGGCC GGCAAGCCCC CGCTCCCCGG GCTCTCGCGG TCGCACGAGG    2102

ATGCTTGGCA CGTACCCCCT GTACATACTT CCCGGGCGCC CAGCATGGAA ATAAAGCACC    2162

CAGCGCTGCC CTGGGCCCCT GCGAGACTGT GATGGTTCTT TCCACGGGTC AGGCCGAGTC    2222

TGAGGCCTGA GTGGCATGAG GGAGGCAGAG CGGGTCCCAC TGTCCCCACA CTGGCCCAGG    2282

CTGTGCAGGT GTGCCTGGGC CGCCTAGGGT GGGGCTCAGC CAGGGGCTGC CCTCGGCAGG    2342

GTGGGGGATT TGCCAGCGTT GCCCTCCCTC CAGCAGCACC TGCCCTGGGC TGGGCCACGG    2402

GAAGCCCTAG GAGCCCCTGG GGACAGACAC ACAGCCCCTG CCTCTGTAGG AGACTGTCCT    2462

GTTCTGTGAG CGCCCTGTCC TCCGACCTCC ATGCCCACTC GGGGGCATGC CTAGTCCATG    2522

TGCGTAGGGA CAGGCCCTCC CTCACCCATC TACCCCCACG GCACTAACCC CTGGCTGTCC    2582

TGCCCAGCCT CGCACCCGCA TGGGGACACA ACCGACTCCG GGGACATGCA CTCTCGGGCC    2642

CTGTGGAGGG ACTGGTGCAG ATGCCCACAC ACACACTCAG TCCAGACCCG TTCAACAAAA    2702

CCCCCGCACT GAGGTTGGCC GGCCACACGG CCACCACACA CACACGTGCA CGCCTCACAC    2762

ACGGAGCCTC ACCCGGGCGA ACTGCACAGC ACCCAGACCA GAGCAAGGTC CTCGCACACG    2822

TGAACACTCC TCGGACACAG GCCCCCACGA GCCCCACGCG GCACCTCAAG GCCCACGAGC    2882

CTCTCGGCAG CTTCTCCACA TGCTGACCTG CTCAGACAAA CCCAGCCCTC CTCTCACAAG    2942

GGTGCCCCTG CAGCCGCCAC ACACACACAG GGGATCACAC ACCACGTCAC GTCCCTGGCC    3002

CTGGCCCACT TCCCAGTGCC GCCCTTCCCT GCAGGGCGGA TCATAATCAG CCATACCACA    3062

TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCCACACC TCCCCCTGAA CCTGAAACAT    3122

AAAATGAATG CAATTGTTGT TGTTAACTTG TTTATTGCAG CTTATAATGG TTACAAATAA    3182

AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT CACTGCATTC TAGTTGTGGT    3242

TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTAGATCC                          3282


(2) INFORMATION FOR SEQ ID NO:155:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 146 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1             5               10              15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20              25              30

Pro Gly Ala Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Arg Phe
        35              40              45

Ser Asn Phe Val Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Phe
    50              55              60

Glu Trp Met Gly Trp Ile Asn Pro Tyr Asn Gly Asn Lys Glu Phe Ser
65              70              75              80

Ala Lys Phe Gln Asp Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn
            85              90              95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala Asp Thr Ala Val
            100             105             110

Tyr Tyr Cys Ala Arg Val Gly Pro Tyr Ser Trp Asp Asp Ser Pro Gln
        115             120             125

Asp Asn Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Ile Val
    130             135             140

Ser Ser
145

(2) INFORMATION FOR SEQ ID NO:156:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 13254 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

TTCATTGATC ATTAATCAGC CATACCACAT TTGTAGAGGT TTTACTTGCT TTAAAAAACC        60

TCCCACACCT CCCCCTGAAC CTGAAACATA AAATGAATGC AATTGTTGTT GTTAACTTGT        120

```
TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTC ACAAATAAAG    180

CATTTTTTTC ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG    240

TCTGGATCTC TAGCTTCGTG TCAAGGACGG TGACTGCAGT GAATAATAAA ATGTGTGTTT    300

GTCCGAAATA CGCGTTTTGA GATTTCTGTC GCCGACTAAA TTCATGTCGC GCGATAGTGG    360

TGTTTATCGC CGATAGAGAT GGCGATATTG GAAAAATCGA TATTTGAAAA TATGGCATAT    420

TGAAAATGTC GCCGATGTGA GTTTCTGTGT AACTGATATC GCCATTTTTC CAAAAGTGAT    480

TTTTGGGCAT ACGCGATATC TGGCGATAGC GCTTATATCG TTTACGGGGG ATGGCGATAG    540

ACGACTTTGG TGACTTGGGC GATTCTGTGT GTCGCAAATA TCGCAGTTTC GATATAGGTG    600

ACAGACGATA TGAGGCTATA TCGCCGATAG AGGCGACATC AAGCTGGCAC ATGGCCAATG    660

CATATCGATC TATACATTGA ATCAATATTG GCCATTAGCC ATATTATTCA TTGGTTATAT    720

AGCATAAATC AATATTGGCT ATTGGCCATT GCATACGTTG TATCCATATC ATAATATGTA    780

CATTTATATT GGCTCATGTC CAACATTACC GCCATGTTGA CATTGATTAT TGACTAGTTA    840

TTAATAGTAA TCAATTACGG GGTCATTAGT TCATAGCCCA TATATGGAGT TCCGCGTTAC    900

ATAACTTACG GTAAATGGCC CGCCTGGCTG ACCGCCCAAC GACCCCCGCC CATTGACGTC    960

AATAATGACG TATGTTCCCA TAGTAACGCC AATAGGGACT TTCCATTGAC GTCAATGGGT   1020

GGAGTATTTA CGGTAAACTG CCCACTTGGC AGTACATCAA GTGTATCATA TGCCAAGTAC   1080

GCCCCCTATT GACGTCAATG ACGGTAAATG GCCCGCCTGG CATTATGCCC AGTACATGAC   1140

CTTATGGGAC TTTCCTACTT GGCAGTACAT CTACGTATTA GTCATCGCTA TTACCATGGT   1200

GATGCGGTTT TGGCAGTACA TCAATGGGCG TGGATAGCGG TTTGACTCAC GGGGATTTCC   1260

AAGTCTCCAC CCCATTGACG TCAATGGGAG TTTGTTTTGG CACCAAAATC AACGGGACTT   1320

TCCAAAATGT CGTAACAACT CCGCCCCATT GACGCAAATG GGCGGTAGGC GTGTACGGTG   1380

GGAGGTCTAT ATAAGCAGAG CTCGTTTAGT GAACCGTCAG ATCGCCTGGA GACGCCATCC   1440

ACGCTGTTTT GACCTCCATA GAAGACACCG GGACCGATCC AGCCTCCGCG GCCGGGAACG   1500

GTGCATTGGA ACGCGGATTC CCCGTGCCAA GAGTGACGTA AGTACCGCCT ATAGAGTCTA   1560

TAGGCCCACC CCCTTGGCTT CTTATGCATG CTATACTGTT TTTGGCTTGG GGTCTATACA   1620

CCCCCGCTTC CTCATGTTAT AGGTGATGGT ATAGCTTAGC CTATAGGTGT GGGTTATTGA   1680
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CCATTATTGA CCACTCCCCT ATTGGTGACG ATACTTTCCA TTACTAATCC ATAACATGGC    1740

TCTTTGCCAC AACTCTCTTT ATTGGCTATA TGCCAATACA CTGTCCTTCA GAGACTGACA    1800

CGGACTCTGT ATTTTTACAG GATGGGGTCT CATTTATTAT TTACAAATTC ACATATACAA    1860

CACCACCGTC CCCAGTGCCC GCAGTTTTTA TTAAACATAA CGTGGGATCT CCACGCGAAT    1920

CTCGGGTACG TGTTCCGGAC ATGGGCTCTT CTCCGGTAGC GGCGGAGCTT CTACATCCGA    1980

GCCCTGCTCC CATGCCTCCA GCGACTCATG GTCGCTCGGC AGCTCCTTGC TCCTAACAGT    2040

GGAGGCCAGA CTTAGGCACA GCACGATGCC CACCACCACC AGTGTGCCGC ACAAGGCCGT    2100

GGCGGTAGGG TATGTGTCTG AAAATGAGCT CGGGGAGCGG GCTTGCACCG CTGACGCATT    2160

TGGAAGACTT AAGGCAGCGG CAGAAGAAGA TGCAGGCAGC TGAGTTGTTG TGTTCTGATA    2220

AGAGTCAGAG GTAACTCCCG TTGCGGTGCT GTTAACGGTG GAGGGCAGTG TAGTCTGAGC    2280

AGTACTCGTT GCTGCCGCGC GCGCCACCAG ACATAATAGC TGACAGACTA ACAGACTGTT    2340

CCTTTCCATG GGTCTTTTCT GCAGTCACCG TCCTTGACAC GAAGCTTGGG CTGCAGGTCG    2400

ATCGACTCTA GAGGATCGAT CCCCGGGCGA GCTCGAATTC GCCGCCACCA TGGAATGGAG    2460

CTGGGTCTTT CTCTTCTTCC TGTCAGTAAC TACAGGTGTC CACTCCCAGG TTCAGCTGGT    2520

TCAGTCCGGG GCTGAGGTGA AGAAGCCTGG GGCCTCAGTG AAGGTTTCTT GTCAGGCTTC    2580

TGGATACAGA TTCAGTAACT TTGTTATTCA TTGGGTGCGC CAGGCCCCCG GACAGAGGTT    2640

TGAGTGGATG GGATGGATCA ATCCTTACAA CGGAAACAAA GAATTTTCAG CGAAGTTCCA    2700

GGACAGAGTC ACCTTTACCG CGGACACATC CGCGAACACA GCCTACATGG AGTTGAGGAG    2760

CCTCAGGTCT GCAGACACGG CTGTTTATTA TTGTGCGAGA GTGGGGCCAT ATAGTTGGGA    2820

TGATTCTCCC CAGGACAATT ATTATATGGA CGTCTGGGGC AAAGGAACCA CGGTCATCGT    2880

GAGCTCAGCT TCCACCAAGG GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC    2940

CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC    3000

GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA    3060

GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC    3120

CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAAAGT    3180

TGGTGAGAGG CCAGCACAGG GAGGGAGGGT GTCTGCTGGA AGCCAGGCTC AGCGCTCCTG    3240

CCTGGACGCA TCCCGGCTAT GCAGCCCCAG TCCAGGGCAG CAAGGCAGGC CCCGTCTGCC    3300

TCTTCACCCG GAGGCCTCTG CCCGCCCCAC TCATGCTCAG GGAGAGGGTC TTCTGGCTTT    3360

TTCCCCAGGC TCTGGGCAGG CACAGGCTAG GTGCCCCTAA CCCAGGCCCT GCACACAAAG    3420

GGGCAGGTGC TGGGCTCAGA CCTGCCAAGA GCCATATCCG GGAGGACCCT GCCCCTGACC    3480

TAAGCCCACC CCAAAGGCCA AACTCTCCAC TCCCTCAGCT CGGACACCTT CTCTCCTCCC    3540

AGATTCGAGT AACTCCCAAT CTTCTCTCTG CAGAGCCCAA ATCTTGTGAC AAAACTCACA    3600

CATGCCCACC GTGCCCAGGT AAGCCAGCCC AGGCCTCGCC CTCCAGCTCA AGGCGGGACA    3660

GGTGCCCTAG AGTAGCCTGC ATCCAGGGAC AGGCCCCAGC CGGGTGCTGA CACGTCCACC    3720

TCCATCTCTC CCTCAGCACC TGAGGCCGCG GGAGGACCAT CAGTCTTCCT CTTCCCCCCA    3780

AAACCCAAGG ACACCCTCAT GATCTCCCGG ACCCCTGAGG TCACATGCGT GGTGGTGGAC    3840

GTGAGCCACG AAGACCCTGA GGTCAAGTTC AACTGGTACG TGGACGGCGT GGAGGTGCAT    3900

AATGCCAAGA CAAAGCCGCG GGAGGAGCAG TACAACAGCA CGTACCGTGT GGTCAGCGTC    3960

CTCACCGTCC TGCACCAGGA CTGGCTGAAT GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC    4020

AAAGCCCTCC CAGCCCCCAT CGAGAAAACC ATCTCCAAAG CCAAAGGTGG GACCCGTGGG    4080

GTGCGAGGGC CACATGGACA GAGGCCGGCT CGGCCCACCC TCTGCCCTGA GAGTGACCGC    4140

TGTACCAACC TCTGTCCCTA CAGGGCAGCC CCGAGAACCA CAGGTGTACA CCCTGCCCCC    4200

ATCCCGGGAT GAGCTGACCA AGAACCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA    4260

TCCCAGCGAC ATCGCCGTGG AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC    4320

CACGCCTCCC GTGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAAGC TCACCGTGGA    4380

CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA    4440

CAACCACTAC ACGCAGAAGA GCCTCTCCCT GTCTCCGGGT AAATGAGTGC GACGGCCGGC    4500

AAGCCCCCGC TCCCCGGGCT CTCGCGGTCG CACGAGGATG CTTGGCACGT ACCCCCTGTA    4560

CATACTTCCC GGGCGCCCAG CATGGAAATA AAGCACCCAG CGCTGCCCTG GCCCCTGCG    4620

AGACTGTGAT GGTTCTTTCC ACGGGTCAGG CCGAGTCTGA GGCCTGAGTG GCATGAGGGA    4680

GGCAGAGCGG GTCCCACTGT CCCCACACTG GCCCAGGCTG TGCAGGTGTG CCTGGGCCGC    4740

CTAGGGTGGG GCTCAGCCAG GGGCTGCCCT CGGCAGGGTG GGGGATTTGC CAGCGTTGCC    4800

CTCCCTCCAG CAGCACCTGC CCTGGGCTGG GCCACGGGAA GCCCTAGGAG CCCCTGGGGA      4860

CAGACACACA GCCCCTGCCT CTGTAGGAGA CTGTCCTGTT CTGTGAGCGC CCTGTCCTCC      4920

GACCTCCATG CCCACTCGGG GGCATGCCTA GTCCATGTGC GTAGGGACAG GCCCTCCCTC      4980

ACCCATCTAC CCCCACGGCA CTAACCCCTG GCTGTCCTGC CCAGCCTCGC ACCCGCATGG      5040

GGACACAACC GACTCCGGGG ACATGCACTC TCGGGCCCTG TGGAGGGACT GGTGCAGATG      5100

CCCACACACA CACTCAGTCC AGACCCGTTC AACAAAACCC CCGCACTGAG GTTGGCCGGC      5160

CACACGGCCA CCACACACAC ACGTGCACGC CTCACACACG GAGCCTCACC CGGGCGAACT      5220

GCACAGCACC CAGACCAGAG CAAGGTCCTC GCACACGTGA ACACTCCTCG GACACAGGCC      5280

CCCACGAGCC CCACGCGGCA CCTCAAGGCC CACGAGCCTC TCGGCAGCTT CTCCACATGC      5340

TGACCTGCTC AGACAAACCC AGCCCTCCTC TCACAAGGGT GCCCCTGCAG CCGCCACACA      5400

CACACAGGGG ATCACACACC ACGTCACGTC CCTGGCCCTG GCCCACTTCC CAGTGCCGCC      5460

CTTCCCTGCA GGGCGGATCA TAATCAGCCA TACCACATTT GTAGAGGTTT TACTTGCTTT      5520

AAAAAACCTC CCACACCTCC CCCTGAACCT GAAACATAAA ATGAATGCAA TTGTTGTTGT      5580

TAACTTGTTT ATTGCAGCTT ATAATGGTTA CAAATAAAGC AATAGCATCA CAAATTTCAC      5640

AAATAAAGCA TTTTTTTCAC TGCATTCTAG TTGTGGTTTG TCCAAACTCA TCAATGTATC      5700

TTATCATGTC TAGATCCTCT ACGCCGGACG CATCGTGGCC GGCATCACCG GCGCCACAGG      5760

TGCGGTTGCT GGCGCCTATA TCGCCGACAT CACCGATGGG GAAGATCGGG CTCGCCACTT      5820

CGGGCTCATG AGCGCTTGTT TCGGCGTGGG TATGGTGGCA GGCCCGTGGC CGGGGGACTG      5880

TTGGGCGCCA TCTCCTTGCA TGCACCATTC CTTGCGGCGG CGGTGCTCAA CGGCCTCAAC      5940

CTACTACTGG GCTGCTTCCT AATGCAGGAG TCGCATAAGG GAGAGCGTCG ACCTCGGGCC      6000

GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC      6060

TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA      6120

AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA CCGGATACCT GTCCGCCTTT      6180

CTCCCTTCGG GAAGCGTGGC GCTTTCTCAA TGCTCACGCT GTAGGTATCT CAGTTCGGTG      6240

TAGGTCGTTC GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC      6300

GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG      6360

GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC    6420

TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG    6480

CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT GATCCGGCAA ACAAACCACC    6540

GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT    6600

CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACTCACGT    6660

TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTAA    6720

AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA CTTGGTCTGA CAGTTACCAA    6780

TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC CATAGTTGCC    6840

TGACTCCCCG TCGTGTAGAT AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT    6900

GCAATGATAC CGCGAGACCC ACGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA    6960

GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT CCGCCTCCAT CCAGTCTATT    7020

AATTGTTGCC GGGAAGCTAG AGTAAGTAGT TCGCCAGTTA ATAGTTTGCG CAACGTTGTT    7080

GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC    7140

GGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC    7200

TCCTTCGGTC CTCCGATCGT TGTCAGAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT    7260

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CCGGCGTCAA CACGGGATAA TACCGCGCCA CATAGCAGAA CTTTAAAAGT GCTCATCATT    7440

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CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCCGCGC    7740

ACATTTCCCC GAAAAGTGCC ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC    7800

TATAAAAATA GGCGTATCAC GAGGCCCTGA TGGCTCTTTG CGGCACCCAT CGTTCGTAAT    7860

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GCGGCTTTGG CAGCCAAGCT AGATCCGGCT GTGGAATGTG TGTCAGTTAG GGTGTGGAAA    8040

GTCCCCAGGC TCCCCAGCAG GCAGAAGTAT GCAAAGCATG CATCTCAATT AGTCAGCAAC    8100

CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCATAG    8160

TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC CAGTTCCGCC CATTCTCCGC    8220

CCCATGGCTG ACTAATTTTT TTATTTATG CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC    8280

TATTCCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AACTAGCTTG    8340

GGGCCACCGC TCAGAGCACC TTCCACCATG GCCACCTCAG CAAGTTCCCA CTTGAACAAA    8400

AACATCAAGC AAATGTACTT GTGCCTGCCC CAGGGTGAGA AAGTCCAAGC CATGTATATC    8460

TGGGTTGATG GTACTGGAGA AGGACTGCGC TGCAAAACCC GCACCCTGGA CTGTGAGCCC    8520

AAGTGTGTAG AAGAGTTACC TGAGTGGAAT TTTGATGGCT CTAGTACCTT TCAGTCTGAG    8580

GGCTCCAACA GTGACATGTA TCTCAGCCCT GTTGCCATGT TTCGGGACCC CTTCCGCAGA    8640

GATCCCAACA AGCTGGTGTT CTGTGAAGTT TTCAAGTACA ACCGGAAGCC TGCAGAGACC    8700

AATTTAAGGC ACTCGTGTAA ACGGATAATG GACATGGTGA GCAACCAGCA CCCCTGGTTT    8760

GGAATGGAAC AGGAGTATAC TCTGATGGGA ACAGATGGGC ACCCTTTTGG TTGGCCTTCC    8820

AATGGCTTTC CTGGGCCCCA AGGTCCGTAT TACTGTGGTG TGGGCGCAGA CAAAGCCTAT    8880

GGCAGGGATA TCGTGGAGGC TCACTACCGC GCCTGCTTGT ATGCTGGGGT CAAGATTACA    8940

GGAACAAATG CTGAGGTCAT GCCTGCCCAG TGGGAACTCC AAATAGGACC CTGTGAAGGA    9000

ATCCGCATGG GAGATCATCT CTGGGTGGCC CGTTTCATCT TCATCGAGTA TGTGAAGACT    9060

TTGGGGTAAT AGCAACCTTT GACCCCAAGC CCATTCCTGG GAACTGGAAT GGTGCAGGCT    9120

GCCATACCAA CTTTAGCACC AAGGCCATGC GGGAGGAGAA TGGTCTGAAG CACATCGAGG    9180

AGGCCATCGA GAAACTAAGC AAGCGGCACC GGTACCACAT TCGAGCCTAC GATCCCAAGG    9240

GGGGCCTGGA CAATGCCCGT GGTCTGACTG GGTTCCACGA AACGTCCAAC ATCAACGACT    9300

TTTCTGCTGG TGTCGCCAAT CGCAGTGCCA GCATCCGCAT TCCCCGGACT GTCGGCCAGG    9360

AGAAGAAAGG TTACTTTGAA GACCGCGGCC CCTCTGCCAA TTGTGACCCC TTTGCAGTGA    9420

CAGAAGCCAT CGTCCGCACA TGCCTTCTCA ATGAGACTGG CCACGAGCCC TTCCAATACA    9480

AAAACTAATT AGACTTTGAG TGATCTTGAG CCTTTCCTAG TTCATCCCAC CCCGCCCCAG    9540

AGAGATCTTT GTGAAGGAAC CTTACTTCTG TGGTGTGACA TAATTGGACA AACTACCTAC    9600

AGAGATTTAA AGCTCTAAGG TAAATATAAA ATTTTTAAGT GTATAATGTG TTAAACTACT    9660

GATTCTAATT GTTTGTGTAT TTTAGATTCC AACCTATGGA ACTGATGAAT GGGAGCAGTG    9720

GTGGAATGCC TTTAATGAGG AAAACCTGTT TTGCTCAGAA GAAATGCCAT CTAGTGATGA    9780

TGAGGCTACT GCTGACTCTC AACATTCTAC TCCTCCAAAA AAGAAGAGAA AGGTAGAAGA    9840

CCCCAAGGAC TTTCCTTCAG AATTGCTAAG TTTTTTGAGT CATGCTGTGT TTAGTAATAG    9900

AACTCTTGCT TGCTTTGCTA TTTACACCAC AAAGGAAAAA GCTGCACTGC TATACAAGAA    9960

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ACTGTTTTTT CTTACTCCAC ACAGGCATAG AGTGTCTGCT ATTAATAACT ATGCTCAAAA    10080

ATTGTGTACC TTTAGCTTTT TAATTTGTAA AGGGGTTAAT AAGGAATATT TGATGTATAG    10140

TGCCTTGACT AGAGATCATA ATCAGCCATA CCACATTTGT AGAGGTTTTA CTTGCTTTAA    10200

AAAACCTCCC ACACCTCCCC CTGAACCTGA AACATAAAAT GAATGCAATT GTTGTTGTTA    10260

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ATAAAGCATT TTTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT    10380

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GTGTTTGTCC GAAATACGCG TTTTGAGATT TCTGTCGCCG ACTAAATTCA TGTCGCGCGA    10500

TAGTGGTGTT TATCGCCGAT AGAGATGGCG ATATTGGAAA AATCGATATT TGAAAATATG    10560

GCATATTGAA AATGTCGCCG ATGTGAGTTT CTGTGTAACT GATATCGCCA TTTTTCCAAA    10620

AGTGATTTTT GGGCATACGC GATATCTGGC GATAGCGCTT ATATCGTTTA CGGGGGATGG    10680

CGATAGACGA CTTTGGTGAC TTGGGCGATT CTGTGTGTCG CAAATATCGC AGTTCGATA    10740

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CCAATGCATA TCGATCTATA CATTGAATCA ATATTGGCCA TTAGCCATAT TATTCATTGG    10860

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TATGTACATT TATATTGGCT CATGTCCAAC ATTACCGCCA TGTTGACATT GATTATTGAC    10980

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GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC ATTGACGTCA    11160

ATGGGTGGAG TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC    11220

AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA    11280

CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC    11340

CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG    11400

ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC AAAATCAACG    11460

GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT    11520

ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG    11580

CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGCGGCCG    11640

GGAACGGTGC ATTGGAACGC GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCCTATAG    11700

AGTCTATAGG CCCACCCCCT TGGCTTCTTA TGCATGCTAT ACTGTTTTTG GCTTGGGGTC    11760

TATACACCCC CGCTTCCTCA TGTTATAGGT GATGGTATAG CTTAGCCTAT AGGTGTGGGT    11820

TATTGACCAT TATTGACCAC TCCCCTATTG GTGACGATAC TTTCCATTAC TAATCCATAA    11880

CATGGCTCTT TGCCACAACT CTCTTTATTG GCTATATGCC AATACACTGT CCTTCAGAGA    11940

CTGACACGGA CTCTGTATTT TTACAGGATG GGGTCTCATT TATTATTTAC AAATTCACAT    12000

ATACAACACC ACCGTCCCCA GTGCCCGCAG TTTTTATTAA ACATAACGTG GGATCTCCAC    12060

GCGAATCTCG GGTACGTGTT CCGGACATGG GCTCTTCTCC GGTAGCGGCG GAGCTTCTAC    12120

ATCCGAGCCC TGCTCCCATG CCTCCAGCGA CTCATGGTCG CTCGGCAGCT CCTTGCTCCT    12180

AACAGTGGAG GCCAGACTTA GGCACAGCAC GATGCCCACC ACCACCAGTG TGCCGCACAA    12240

GGCCGTGGCG GTAGGGTATG TGTCTGAAAA TGAGCTCGGG GAGCGGGCTT GCACCGCTGA    12300

CGCATTTGGA AGACTTAAGG CAGCGGCAGA AGAAGATGCA GGCAGCTGAG TTGTTGTGTT    12360

CTGATAAGAG TCAGAGGTAA CTCCCGTTGC GGTGCTGTTA ACGGTGGAGG GCAGTGTAGT    12420

CTGAGCAGTA CTCGTTGCTG CCGCGCGCGC CACCAGACAT AATAGCTGAC AGACTAACAG    12480

ACTGTTCCTT TCCATGGGTC TTTTCTGCAG TCACCGTCCT TGACACGAAG CTTACCATGG    12540

GTGTGCCCAC TCAGGTCCTG GGGTTGCTGC TGCTGTGGCT TACAGATGCC AGATGTGAGA    12600

TCGTTCTCAC GCAGTCTCCA GGCACCCTGT CTCTGTCTCC AGGGGAAAGA GCCACCTTCT    12660

CCTGTAGGTC CAGTCACAGC ATTCGCAGCC GCCGCGTAGC CTGGTACCAG CACAAACCTG    12720

GCCAGGCTCC AAGGCTGGTC ATACATGGTG TTTCCAATAG GGCCTCTGGC ATCTCAGACA    12780

GGTTCAGCGG CAGTGGGTCT GGGACAGACT TCACTCTCAC CATCACCAGA GTGGAGCCTG    12840

AAGACTTTGC ACTGTACTAC TGTCAGGTCT ATGGTGCCTC CTCGTACACT TTTGGCCAGG    12900

GGACCAAACT GGAGAGGAAA CGAACTGTGC CTGCACCATC TGTCTTCATC TTCCCGCCAT    12960

CTGATGAGCA GTTGAAATCT GGGACTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC    13020

CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG    13080

AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC    13140

TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC CATCAGGGCC    13200

TGAGATCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG TTAATTCTAG AGAA    13254

(2) INFORMATION FOR SEQ ID NO:157:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CAGGTTCAGC TGGTTCAGTC CGGGGCT                                          27

(2) INFORMATION FOR SEQ ID NO:158:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCTTGGAGCT CACGATGACC GTGGTTCCTT GGCCCCAGAC GTCC                    44

(2) INFORMATION FOR SEQ ID NO:159:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGCCGCGAAT TCGCCGCCAC CATGGAATGG AGCTGGGTCT TTCTCTTCTT CCTGTCAGTA        60


(2) INFORMATION FOR SEQ ID NO:160:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

AGCCCCGGAC TGAACCAGCT GAACCTG                                       27

(2) INFORMATION FOR SEQ ID NO:161:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GGAGTTGAGG AGCCTCAGGT CTGCAGACAC GG                                 32

(2) INFORMATION FOR SEQ ID NO:162:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CCGTGTCTGC AGACCTGTGG CTCCTCAACT CC                                         32

(2) INFORMATION FOR SEQ ID NO:163:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATGCCAGAT GTGAGATCGT TCTCACGCAG TCT                                        33

(2) INFORMATION FOR SEQ ID NO:164:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 67 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GCGGGATCCG AATTCTCTAG AATTAACACT CTCCCCTGTT GAAGCTCTTT GTGACGGGCG          60

AACTCAG                                                                    67

(2) INFORMATION FOR SEQ ID NO:165:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 51 base pairs

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCGCGAATTC ACCATGGGTG TGCCCACTCA GGTCCTGGGG GTTGCTGCTG C                    51

(2) INFORMATION FOR SEQ ID NO:166:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

AGACTGCGTG AGAACGATCT CACATCTGGC ATC                    33

(2) INFORMATION FOR SEQ ID NO:167:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GCGCAAGCTT ACCATGGGTG TGCCCACTCA GGTCCTGGGG TTGCTGCTGC                    50

(2) INFORMATION FOR SEQ ID NO:168:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 729 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```
GAATTCTCTA GAATTAACAC TCTCCCCTGT TGAAGCTCTT TGTGACGGGC GAACTCAGGC      60

CCTGATGGGT GACTTCGCAG GCGTAGACTT TGTGTTTCTC GTAGTCTGCT TTGCTCAGCG     120

TCAGGGTGCT GCTGAGGCTG TAGGTGCTGT CCTTGCTGTC CTGCTCTGTG ACACTCTCCT     180

GGGAGTTACC CGATTGGAGG GCGTTATCCA CCTTCCACTG TACTTTGGCC TCTCTGGGAT     240

AGAAGTTATT CAGCAGGCAC ACAACAGAGG CAGTCCCAGA TTTCAACTGC TCATCAGATG     300

GCGGGAAGAT GAAGACAGAT GGTGCAGGCA CAGTTCGTTT CCTCTCCAGT TTGGTCCCCT     360

GGCCAAAAGT GTACGAGGAG GCACCATAGA CCTGACAGTA GTACAGTGCA AAGTCTTCAG     420

GCTCCACTCT GGTGATGGTG AGAGTGAAGT CTGTCCCAGA CCCACTGCCG CTGAACCTGT     480

CTGAGATGCC AGAGGCCCTA TTGGAAACAC CATGTATGAC CAGCCTTGGA GCCTGGCCAG     540

GTTTGTGCTG GTACCAGGCT ACGCGGCGGC TGCGAATGCT GTGACTGGAC CTACAGGAGA     600

AGGTGGCTCT TTCCCCTGGA GACAGAGACA GGGTGCCTGG AGACTGCGTG AGAACGATCT     660

CACATCTGGC ATCTGTAAGC CACAGCAGCA GCAACCCCAG GACCTGAGTG GGCACACCCA     720

TGGTAAGCT                                                             729
```

(2) INFORMATION FOR SEQ ID NO:169:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 3282 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```
GGATCTAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAACTA GAATGCAGTG      60

AAAAAAATGC TTTATTTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA CCATTATAAG     120

CTGCAATAAA CAAGTTAACA ACAACAATTG CATTCATTTT ATGTTTCAGG TTCAGGGGGA     180
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GGTGTGGGAG GTTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTATGG CTGATTATGA    240

TCCGCCCTGC AGGGAAGGGC GGCACTGGGA AGTGGGCCAG GGCCAGGGAC GTGACGTGGT    300

GTGTGATCCC CTGTGTGTGT GTGGCGGCTG CAGGGGCACC CTTGTGAGAG GAGGGCTGGG    360

TTTGTCTGAG CAGGTCAGCA TGTGGAGAAG CTGCCGAGAG GCTCGTGGGC CTTGAGGTGC    420

CGCGTGGGGC TCGTGGGGGC CTGTGTCCGA GGAGTGTTCA CGTGTGCGAG GACCTTGCTC    480

TGGTCTGGGT GCTGTGCAGT TCGCCCGGGT GAGGCTCCGT GTGTGAGGCG TGCACGTGTG    540

TGTGTGGTGG CCGTGTGGCC GGCCAACCTC AGTGCGGGGG TTTTGTTGAA CGGGTCTGGA    600

CTGAGTGTGT GTGTGGGCAT CTGCACCAGT CCCTCCACAG GGCCCGAGAG TGCATGTCCC    660

CGGAGTCGGT TGTGTCCCCA TGCGGGTGCG AGGCTGGGCA GGACAGCCAG GGGTTAGTGC    720

CGTGGGGGTA GATGGGTGAG GGAGGGCCTG TCCCTACGCA CATGGACTAG GCATGCCCCC    780

GAGTGGGCAT GGAGGTCGGA GGACAGGGCG CTCACAGAAC AGGACAGTCT CCTACAGAGG    840

CAGGGGCTGT GTGTCTGTCC CCAGGGGCTC CTAGGGCTTC CCGTGGCCCA GCCCAGGGCA    900

GGTGCTGCTG GAGGGAGGGC AACGCTGGCA AATCCCCCAC CCTGCCGAGG GCAGCCCCTG    960

GCTGAGCCCC ACCCTAGGCG GCCCAGGCAC ACCTGCACAG CCTGGGCCAG TGTGGGGACA   1020

GTGGGACCCG CTCTGCCTCC CTCATGCCAC TCAGGCCTCA GACTCGGCCT GACCCGTGGA   1080

AAGAACCATC ACAGTCTCGC AGGGGCCCAG GGCAGCGCTG GGTGCTTTAT TTCCATGCTG   1140

GGCGCCCGGG AAGTATGTAC AGGGGGTACG TGCCAAGCAT CCTCGTGCGA CCGCGAGAGC   1200

CCGGGGAGCG GGGGCTTGCC GGCCGTCGCA CTCATTTACC CGGAGACAGG GAGAGGCTCT   1260

TCTGCGTGTA GTGGTTGTGC AGAGCCTCAT GCATCACGGA GCATGAGAAG ACGTTCCCCT   1320

GCTGCCACCT GCTCTTGTCC ACGGTGAGCT TGCTGTAGAG GAAGAAGGAG CCGTCGGAGT   1380

CCAGCACGGG AGGCGTGGTC TTGTAGTTGT CTCCGGCTG CCCATTGCTC TCCCACTCCA   1440

CGGCGATGTC GCTGGGATAG AAGCCTTTGA CCAGGCAGGT CAGGCTGACC TGGTTCTTGG   1500

TCAGCTCATC CCGGGATGGG GGCAGGGTGT ACACCTGTGG TTCTCGGGGC TGCCCTGTAG   1560

GGACAGAGGT TGGTACAGCG GTCACTCTCA GGGCAGAGGG TGGGCCGAGC CGGCCTCTGT   1620

CCATGTGGCC CTCGCACCCC ACGGGTCCCA CCTTTGGCTT TGGAGATGGT TTTCTCGATG   1680

GGGGCTGGGA GGGCTTTGTT GGAGACCTTG CACTTGTACT CCTTGCCATT CAGCCAGTCC   1740
```

TGGTGCAGGA CGGTGAGGAC GCTGACCACA CGGTACGTGC TGTTGTACTG CTCCTCCCGC    1800

GGCTTTGTCT TGGCATTATG CACCTCCACG CCGTCCACGT ACCAGTTGAA CTTGACCTCA    1860

GGGTCTTCGT GGCTCACGTC CACCACCACG CATGTGACCT CAGGGGTCCG GGAGATCATG    1920

AGGGTGTCCT TGGGTTTTGG GGGGAAGAGG AAGACTGATG GTCCTCCCGC GGCCTCAGGT    1980

GCTGAGGGAG AGATGGAGGT GGACGTGTCA GCACCCGGCT GGGGCCTGTC CCTGGATGCA    2040

GGCTACTCTA GGGCACCTGT CCCGCCTTGA GCTGGAGGGC GAGGCCTGGG CTGGCTTACC    2100

TGGGCACGGT GGGCATGTGT GAGTTTTGTC ACAAGATTTG GGCTCTGCAG AGAGAAGATT    2160

GGGAGTTACT CGAATCTGGG AGGAGAGAAG GTGTCCGAGC TGAGGGAGTG GAGAGTTTGG    2220

CCTTTGGGGT GGGCTTAGGT CAGGGGCAGG GTCCTCCCGG ATATGGCTCT TGGCAGGTCT    2280

GAGCCCAGCA CCTGCCCCTT TGTGTGCAGG GCCTGGGTTA GGGGCACCTA GCCTGTGCCT    2340

GCCCAGAGCC TGGGGAAAAA GCCAGAAGAC CCTCTCCCTG AGCATGAGTG GGGCGGGCAG    2400

AGGCCTCCGG GTGAAGAGGC AGACGGGGCC TGCCTTGCTG CCCTGGACTG GGGCTGCATA    2460

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TGCAGATGTA GGTCTGGGTG CCCAAGCTGC TGGAGGGCAC GGTCACCACG CTGCTGAGGG    2640

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TGTCCTGGGG AGAATCATCC CAACTATATG GCCCCACTCT CGCACAATAA TAAACAGCCG    2940

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TAAAGGTGAC TCTGTCCTGG AACTTCGCTG AAAATTCTTT GTTTCCGTTG TAAGGATTGA    3060

TCCATCCCAT CCACTCAAAC CTCTGTCCGG GGGCCTGGCG CACCCAATGA ATAACAAAGT    3120

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CCTCAGCCCC GGACTGAACC AGCTGAACCT GGGAGTGGAC ACCTGTAGTT ACTGACAGGA    3240

AGAAGAGAAA GACCCAGCTC CATTCCATGG TGGCGGCGAA TT                       3282

(2) INFORMATION FOR SEQ ID NO:170:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13254 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

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AGTTACCCGA TTGGAGGGCG TTATCCACCT TCCACTGTAC TTTGGCCTCT CTGGGATAGA     240

AGTTATTCAG CAGGCACACA ACAGAGGCAG TCCCAGATTT CAACTGCTCA TCAGATGGCG     300

GGAAGATGAA GACAGATGGT GCAGGCACAG TTCGTTTCCT CTCCAGTTTG GTCCCCTGGC     360

CAAAAGTGTA CGAGGAGGCA CCATAGACCT GACAGTAGTA CAGTGCAAAG TCTTCAGGCT     420

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AAGATACATT GATGAGTTTG GACAAACCAC AACTAGAATG CAGTGAAAAA AATGCTTTAT   13080

TTGTGAAATT TGTGATGCTA TTGCTTTATT TGTAACCATT ATAAGCTGCA ATAAACAAGT   13140

TAACAACAAC AATTGCATTC ATTTTATGTT TCAGGTTCAG GGGGAGGTGT GGGAGGTTTT   13200

TTAAAGCAAG TAAAACCTCT ACAAATGTGG TATGGCTGAT TAATGATCAA TGAA         13254